

PD 09-NOV-1994; 305433.
 PF 18-MAY-1990; US-355027.
 PR 19-MAY-1989; US-355027.
 PR 29-MAR-1990; US-501904.
 PA (AMGE-) AMGEN INC.
 PA (CHIL-) CHILDREN'S HOSPITAL LOS ANGELES.
 PI Boone TC, Declerck YA, Langley KE;
 WP1; 94-34330943.
 DR N-PSDB; 073088.
 PT New metallo-proteinase inhibitor, analogues and DNA - for
 PT treating tumour cell dissemination, rheumatoid arthritis and for
 PT large-scale recombinant inhibitor prodn.
 PS Claim 8; Fig 2; 65pp; English.
 CC Q73088 encodes R62769 human metalloproteinase inhibitor (MI), it
 CC may be used to inhibit tumour cell dissemination and for treating
 CC rheumatoid arthritis, dystrophic epidermolysis bullosa, emphysema
 CC and osteoporosis. The DNA may be used to detect MI gene disorders.
 SQ Sequence 220 AA;

DB 12; Score 220; Matches 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1 maaartirlalglillat1rpadacspsphqgchadvirakavsekevdsgnd 60
 QY 1 MGAARTIRLALGLILLAT1RLPADACSCSPHPQQFCNADVVIRAKAVSEKEVDSGND 60
 DB 61 iygnpikrqyeikqkmfkgekdfiytypassavcgvslvdggkeyiagkaegdg 120
 QY 61 IYGNPIKRQYEIKQKMFKGEKDFIYTAPSSAVCGVSLVDGKEYIAGKAEGDG 120
 DB 121 kmhitlclfivpwt1sttqksslhrqymgeckitrcpmcyisspdec1wmdwte 180
 QY 121 KMHITLCLDFIVPWT1STTQKSSLHRQYQMCCECKITRCMPCYISSPDEC1WMDWTE 180
 DB 121 kningqakffaci1rsgcawrygaappkqef1iedp 220
 QY 121 KNINGHQAKFFACIKRSDGSCAWRYGAAPPKQEF1IEDP 220

RESULT 2
 ID R07955 standard; protein; 220 AA.
 AC R07955.
 DT 21-FEB-1991 (first entry)
 DE Human metalloproteinase inhibitor gene product.
 KW Tumour; chemotherapy; cancer; Page's disease; osteoporosis;
 KW scleroderma; cholesteatoma.
 OS Homo sapiens.
 FT Protein
 PN EP-398753-A.
 PR 18-MAY-1990; 305433.
 PR 19-MAY-1989; US-355027.
 PR 29-MAR-1990; US-501904.
 PA (AMGE-) AMGEN INC.
 PA (CHIL-) CHILDREN'S HOSPITAL OF LA.
 PI Langley KE, Boone TC, DeClerck YA;
 DR WP1; 90-350481/47.
 DR N-PSDB; 006584.
 PT New metallo-proteinase inhibitor polypeptide(s) - and DNA

PT encoding them, for treatment of tumour cell dissemination and
 PT rheumatoid arthritis.
 Claim 12; Fig 2; 63pp; English.
 The product has therapeutic use in inhibiting tumour dissemination
 CC during chemotherapy and radiation therapy, impurged bone marrow cell
 CC harvesting etc. The inhibitor may also be useful in encapsulating
 CC tumours aiding clean excision, and in treatment of emphysema, Page's
 CC disease, osteoporosis, scleroderma and bedsores.
 The gene product also has application in autoimmune disorders eg.
 CC rheumatoid arthritis and multiple sclerosis.
 CC
 See also Q0583.
 Sequence 220 AA;

DB 2; Score 1643; Match 100.0%; QryMatch 100.0%; Pred. No. 1.02e-170;
 DB Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1 maaartirlalglillat1rpadacspsphqgchadvirakavsekevdsgnd 60
 QY 1 MGAARTIRLALGLILLAT1RLPADACSCSPHPQQFCNADVVIRAKAVSEKEVDSGND 60
 DB 61 iygnpikrqyeikqkmfkgekdfiytypassavcgvslvdggkeyiagkaegdg 120
 QY 61 IYGNPIKRQYEIKQKMFKGEKDFIYTAPSSAVCGVSLVDGKEYIAGKAEGDG 120
 DB 121 kmhitlclfivpwt1sttqksslhrqymgeckitrcpmcyisspdec1wmdwte 180
 QY 121 KMHITLCLDFIVPWT1STTQKSSLHRQYQMCCECKITRCMPCYISSPDEC1WMDWTE 180
 DB 181 kningqakffaci1rsgcawrygaappkqef1iedp 220
 QY 181 KNINGHQAKFFACIKRSDGSCAWRYGAAPPKQEF1IEDP 220

RESULT 3
 ID R07954 standard; protein; 220 AA.
 AC R07954.
 DT 21-FEB-1991 (first entry)
 DE Bovine metalloproteinase inhibitor gene product.
 KW Tumour; chemotherapy; cancer; Page's disease; osteoporosis;
 KW scleroderma; cholesteatoma.
 OS Bos taurus.
 FT Protein
 PN EP-398753-A.
 PR 22-NOV-1990; 305433.
 PR 18-MAY-1990; US-501904.
 PR 19-MAY-1989; US-55027.
 PR 29-MAR-1990; US-501904.
 PA (AMGE-) AMGEN INC.
 PA (CHIL-) CHILDREN'S HOSPITAL OF LA.
 PI Langley KE, Boone TC, DeClerck YA;
 DR WP1; 90-350481/47.
 DR N-PSDB; Q06583.
 PT New metallo-proteinase inhibitor polypeptide(s) - and DNA
 PT encoding them, for treatment of tumour cell dissemination and
 PT rheumatoid arthritis.
 Claim 12; Fig 1; 63pp; English.
 The product has therapeutic use in inhibiting tumour dissemination
 CC during chemotherapy and radiation therapy, impurged bone marrow cell
 CC harvesting etc. The inhibitor may also be useful in encapsulating

CC tumours aiding clean excision, and in treatment of emphysema, Paget's disease, osteoporosis, scleroderma and bendois. The gene product also has application in autoimmune disorders eg. rheumatoid arthritis and multiple sclerosis. See also Q6584.

SQ Sequence 220 AA;

DB 2; Score 1550; Match 91.8%; QryMatch 94.3%; Pred. No. 4.04e-160; Matches 202; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

DB 1 maaarsplafacillgtlpradacspphpqafcnadivirakavnkkevdsgnd 60
Matches 12; Mismatches 6; Indels 0; Gaps 0;

QY 1 MGAARTIRLAIGLILLATLIRPADACSCSPVHPQQAFCNADIVIRAKAVSEEVDSGND 60

DB 1 maaarsplafacillgtlpradacspphpqafcnadivirakavnkkevdsgnd 60
Matches 12; Mismatches 6; Indels 0; Gaps 0;

QY 1 MGAARTIRLAIGLILLATLIRPADACSCSPVHPQQFCNADIVIRAKAYSEEVDSGND 60

DB 61 iygnpikrioyekqikmfpkpdqieflytapaasavcgvslldigggkeylaekaeing 120
Matches 12; Mismatches 6; Indels 0; Gaps 0;

QY 61 IYGNPIKRIQYEIKQIKMFPKEPDLEFIYATPSSAVGVSLDVGGKEYLGAEGDG 120

DB 121 nmhltclcdflypwtltsaqkkslnhryqmcgeckitrcpmcyisspdec1wmdwre 180
Matches 12; Mismatches 6; Indels 0; Gaps 0;

QY 121 KMHLTLCDFLYPWTLSTTOKSKSLNHRYQMCGECKITRCPMCYISSPDEC1WMDWRE 180

DB 181 kninghakffaciakrsdgscawyrgaappkqefidelp 220
Matches 12; Mismatches 6; Indels 0; Gaps 0;

QY 181 KNINGHQAKEFACIKRSDFGSCAWYRGAPPKQEFIDELP 220

DB 121 nmhltclcdflypwtltsaqkkslnhryqmcgeckitrcpmcyisspdec1wmdwre 180
Matches 12; Mismatches 6; Indels 0; Gaps 0;

QY 121 KMHLTLCDFLYPWTLSTTOKSKSLNHRYQMCGECKITRCPMCYISSPDEC1WMDWRE 180

DB 181 kninghakffaciakrsdgscawyrgaappkqefidelp 220
Matches 12; Mismatches 6; Indels 0; Gaps 0;

QY 181 KNINGHQAKEFACIKRSDFGSCAWYRGAPPKQEFIDELP 220

RESULT 5
ID R0698 standard; protein; 194 AA.
AC R0698;
DT 16-JAN-1991 (first entry)
DE Complete sequence of human TIMP-2 from clone pSS38.
KW matrix metalloproteinase inhibitor; TIMP-2; pSS38.
OS Synthetis.
PN US494196-A.
PD 21-AUG-1990.
PF 13-MAR-1990; 494796.
PR 21-MAR-1989; US-326334.
PS 17-JUL-1989; US-380431.
DISCLOSURE; Fig 7; 54pp; English.
CC TIMP-2 was isolated from human melanoma cell-conditioned media and the amino acid sequence determined. A probe was synthesised based upon the protein sequence information. It was used to screen a LambdaGem-4 cDNA library prepared from human melanoma cells. 239 positive were identified from a total of 750,000 plaques screened. Further analysis and screening with additional probes eliminated most of the clones. Clone pSS38 was isolated and the nucleotide sequence of the cDNA insert was determined. The deduced amino acid sequence showed excellent agreement with that derived by directly sequencing the TIMP-2 protein.
CC See also Q05937, R06746-R06750, R06894-R06895 and Q05938-Q05939.
SQ Sequence 194 AA;

DR N-PSDB: Q05940.
PT New matrix metallo-proteinase inhibitor - used to treat diseases resulting from matrix metallo-proteinase activity and in diagnosis, detection and purification.

PT Disclosure; Fig 7; 54pp; English.

CC TIMP-2 was isolated from human melanoma cell-conditioned media and the amino acid sequence determined. A probe was synthesised based upon the protein sequence information. It was used to screen a LambdaGem-4 cDNA library prepared from human melanoma cells. 239 positive were identified from a total of 750,000 plaques screened. Further analysis and screening with additional probes eliminated most of the clones. Clone pSS38 was isolated and the nucleotide sequence of the cDNA insert was determined. The deduced amino acid sequence showed excellent agreement with that derived by directly sequencing the TIMP-2 protein.
CC See also Q05937, R06746-R06750, R06894-R06895 and Q05938-Q05939.

DB 2; Score 1454; Match 99.5%; QryMatch 88.5%; Pred. No. 3.40e-149; Matches 193; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 1 cscspvhppqafcnadivirakavsekevdsgndiygnpikrioyekqikmfpkpedi 60
Matches 27; CSGSPVHPQQAFCNADIVIRAKAVSEEVDSGNDIYGNPIKRIQYEIKQIKMFPKPEKDI 60

61 efityapsseavgvslavggkeyliaqkagdgkmhltlcfivpwtl1sttqkkslnh 120
 Db 121 kitrcpmipyisspdec1wmwdwteknighqakffacikrsdgscawyrgaappkgef 180
 Qy 122 KITRCPMIPYISSPDEC1WMWDWTEKNIGHQAKFFACIKRSDGSACAWYRGAPPKQEF 214
 87 EFiTAPSSAVGVSLSLGGKEYLIAQKAGDGKMHLTLCFIVPWTLSLTQKSLNH 146

Db 121 ryqmgceckitrcpmipyisspdec1wmwdwteknighqakffacikrsdgscawyrg 180
 Qy 147 RYQMGCECKITRCPMIPYISSPDEC1WMWDWTEKNIGHQAKFFACIKRSDGSACAWYRG 206

Db 181 aappkqefldiedp 194
 Qy 207 AAPPKQEFLDIEDP 220

RESULT⁶
 ID R06896 standard; protein; 186 AA.
 AC R06896;
 DT 16-JAN-1991 (first entry)
 DE Part of TIMP-2 metalloproteinase inhibitor, encoded by clone pss15.
 KW matrix metalloproteinase inhibitor; TIMP-2; pss15.
 OS Synthetic.
 PN US7494796-A.
 PD 21-AUG-1990; 494796.
 PF 13-MAR-1990; 494796.
 DR 17-JUL-1989; US-326334.
 PT New matrix metallo-proteinase inhibitor - used to treat diseases resulting from matrix metallo-proteinase activity and in diagnosis, detection or therapy.
 PA (USSH) NAT. INST. OF HEALTH.
 PI Stetler-Seenson WG, Liotta LA, Krutzsch HC;
 CC Protein was isolated from human melanoma cell-conditioned media by gelatin-affinity chromatography.
 DR 90-290097/38.
 PT New matrix metallo-proteinase inhibitor - used to treat diseases resulting from matrix metallo-proteinase activity and in diagnosis, detection and purification.
 PT resulting from human melanoma cell-conditioned media and diagnosis, detection and purification.
 PS Disclosure; Fig 6A; 54pp; English.
 CC TIMP-2 was isolated from human melanoma cell-conditioned media and the amino acid sequence determined. A probe was synthesised based upon the protein sequence information. It was used to screen a Lambda^{gt}-4 cDNA library prepared from human melanoma cells. 239 positives were identified from a total of 750 000 plaques screened. Further analysis and screening with additional probes eliminated all but two clones (pss15 and pss18). Both were sequenced and found to encode CSC-21K (=TIMP-2), a novel metalloproteinase inhibitor. This is the amino acid sequence deduced from the cDNA sequence of pss15.
 CC See also Q05937, R06746-R06750, R06894-R06895 and Q05939-Q05940.
 SQ 186 AA;

DB 2; Score 1396; Match 99.5%; OryMatch 85.0%; Pred. No. 1.34e-142;
 Matches 185; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 qqafcnadvvirkavsnkeydsgndiygnpikriyveikdikmfpkpekdiefiyaps 60
 Qy 35 QQACCNADVVIRKAVSEKEVDSGNDIYGNPKRIQEIKQKMPKPEKDIEFLYAPS 94

Db 61 savogsvlavggkeyliaqkagdgkmhltlcfivpwtl1sttqkkslnhrgmgec 120
 Qy 95 SAVOGSVLAVGGKEYLIAQKAGDGKMHLTLCFIVPWTLSLTQKSLNHRYQMGEC 154

Db 121 kitrcpmipyisspdec1wmwdwteknighqakffacikrsdgscawyrgaappkgef 180
 Qy 155 KITRCPMIPYISSPDEC1WMWDWTEKNIGHQAKFFACIKRSDGSACAWYRGAPPKQEF 214
 Db 181 lidiedp 186
 Qy 215 LIDEDP 220

RESULT⁷
 ID R06895 standard; protein; 192 AA.
 AC R06895;
 DT 16-JAN-1991 (first entry)
 DE Metalloproteinase inhibitor TIMP-2.
 KW matrix metalloproteinase inhibitor; TIMP-2 (CSC-21K).
 OS Synthetic.
 PN US7494796-A.
 PD 21-AUG-1990.
 PF 13-MAR-1990; 494796.
 DR 21-MAR-1989; US-326334.
 PR 17-JUL-1989; US-380431.
 PR 18-AUG-1989; US-395453.
 PR 13-MAR-1990; US-494796.
 PA (USSH) NAT. INST. OF HEALTH.
 PI Stetler-Seenson WG, Liotta LA, Krutzsch HC;
 CC Protein was isolated from human melanoma cell-conditioned media by gelatin-affinity chromatography.
 DR 90-290097/38.
 PT New matrix metallo-proteinase inhibitor - used to treat diseases such as arthritis, diabetes, cancer, ulcers of mucosa and epithelial tissues, autoimmune-mediated inflammation, lung injury, granulomatous diseases and myocardial infarctions. It can also be used as a birth control agent by preventing embryo/placental attachment or invasion. Other therapeutic benefits may also be observed in diseases with basement destruction or myocyte destruction. See also Q05937, R06746-R06750, R06894 and Q05938-Q05940.
 SQ Sequence 192 AA;

DB 2; Score 1377; Match 96.4%; OryMatch 83.8%; Pred. No. 1.93e-140;
 Matches 186; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

Db 1 ccspsvhpqgafcnadvvirakavsekevdgndiygnpikriyveikdikmfpkpekdiefiyaps 60
 Qy 27 CSOSPVHPQGAFCNADVVIRKAVSEKEVDSGNDIYGNPKRIQEIKQKMPKPEKDIEFLYAPS 94

Db 61 effiyatpsavgyelvvggkeyliaqkagdgkmhltlcfivpwtl1sttqkkslnh 119
 Qy 87 EFiTAPSSAVGVSLSLGGKEYLIAQKAGDGKMHLTLCFIVPWTLSLTQKSLNH 146

Db 120 Iqggceckitrcpmipcyisspdec1wmwdwteknighqakffacikrsdgscawyrg 179
 Qy 147 RYQMGCECKITRCPMIPCYISSPDEC1WMWDWTEKNIGHQAKFFACIKRSDGSACAWYRG 206

Db 180 aappkqefldiedp 192
 Qy 207 AAPPKQEFLDIEDP 219

RESULT 8
 ID R06897 standard; protein; 177 AA.
 AC E6897;
 DT 16-JAN-1991 (first entry)
 DE Part of TIMP-2 metalloproteinase inhibitor, encoded by clone pSS18.
 KW matrix metalloproteinase inhibitor; TIMP-2; pSS18.
 OS Synthetic.
 PN US7496796-A.
 PD 21-AUG-1990.
 PF 13-MAR-1990; 494796.
 PR 21-MAR-1989; US-322634.
 PR 17-JUL-1989; US-389431.
 PR 18-AUG-1989; US-392453.
 PR 13-MAR-1990; US-494796.
 PA (USSH) NATL INST OF HEALTH.
 PI Stetler-Seenson WG, Liotta LA, Krutzsch HC;
 DR WPI; 90-290097/38.
 DR N-PSDB; 005939.
 PT New matrix metallo-proteinase inhibitor - used to treat diseases
 PT resulting from matrix metallo-proteinase activity and in
 PT diagnosis, detection and purification.
 PS Fig. 6B; 54pp; English.
 CC TIMP-2 was isolated from human melanoma cell-conditioned media and
 CC the amino acid sequence determined. A probe was synthesised
 CC based upon the protein sequence information. It was used to screen
 CC a Lambdagem-4 cDNA library prepared from human melanoma cells. 239
 CC Positive were identified from a total of 750,000 plaques screened.
 CC Further analysis and screening with additional probes eliminated
 CC all but two clones (pSS15 and pSS18). Both were sequenced and found
 CC to encode CSC-21K (=TIMP-2), a novel metalloproteinase inhibitor.
 CC This is the amino acid sequence deduced from the cDNA sequence of
 CC pSS18.
 CC See also Q05937, R06746-R06750, R06894-R06895, Q05938 and Q05940.
 SQ Sequence 177 AA;

DB 2; Score 1337; Match 100.0%; QryMatch 81.4%; Pred. No. 6.73e-136;
 Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 virakavsekevdsgndiygnpikrigrayekikmkgpkediefiytapsavcgvsl 60
 Qy 44 VIRAKAVSEKEVDGNDIYGNPKRIGEIKIKMKGPKEDIEFYTAPSSAVCGVSL 103

Db 61 vggkeyliagaekaegdgmhltlcfdfyprwdtlsttqkkslnhryqmgceokitrcpmip 120
 Qy 104 VGGKEYLIAGKAEGDGMHLTLCDFIVPWTDLSTTQKKSINHRYQMGCEKITRCPMIP 163

Db 121 cyisspdeclwmawtvekninghqakffaciaksdgcamygaapkqgefildedp 177
 Qy 164 CYISSPDECWMWDTVEKNINGHQAKFFACIKRSRDGSCAWTRGARPKQEFILDIEDP 220

RESULT 9
 ID E60786 standard; Protein; 207 AA.
 AC E60786;
 DT 08-AUG-1991 (first entry)
 DE Sequence of tissue inhibitor of metalloproteinase (TIMP).
 KW Connective tissue; extracellular matrix.
 OS Homo sapiens.

Key FH Location/qualifiers
 Peptide signal 1...23
 PR /label= signal 24..207
 PR Protein 24..207
 PR Modified -site 53..55
 PR /label= potential N-glycosylation site
 PR Modified -site 101..103
 PR /label= as above
 PN GB216925-A.
 PD 09-TUL-1986.
 PR 06-JAN-1986; 000199.
 PR 05-OCT-1983; BE-197924.
 PR 07-JAN-1985; GB-000341.
 PR 07-JAN-1985; GB-500341.
 PR 01-NOV-1985; GB-026951.
 PR 06-JAN-1986; GB-000199.
 PA (CELL-) CELLETECH LTD.
 PI Harris TJR, Reynolds JJ, Docherty AJP, Murphy G;
 DR WPI; 86-177873/28.
 DR N-PSDB; N60538.
 PT Prod'n. of metallo-proteinase inhibitors - by recombinant DNA
 PT techniques
 PS Disclosure; Fig 3; 15pp; English.
 CC A gene with residues 64-684 of N60538 is claimed. N60538 was
 CC isolated from human a foetal diploid lung cells (ATCC CCL153) cDNA
 CC library using N60539.
 SQ Sequence 207 AA;

DB 3; Score 521; Match 41.1%; QryMatch 31.7%; Pred. No. 2.50e-44;
 Matches 81; Conservative 39; Mismatches 70; Indels 7; Gaps 7;
 DB 7 lasgillllwiapsractcyphptafcnstlvirakfvgtpevnqt-lygryeikm 65
 QY 10 LAIGLLIATLIRPADACSCSPVHPQQACFNAVDIRAKAYSEKVDSGNDIYGN-PIKR 68

DB 66 tk-mykfqgal-gdaadairfyytpamesvcqyfrhrshnreeffiaglkq-dgllhitr 122
 QY 69 IYVEIKQIKMKGPKEDIEFYTAPSSAVCGVSLDVGGKKE-YLIAGKABGGKHKITC 127

DB 123 sfrapwnslslagrrgftktvtygcectvfpclspcklgqgthclwrcqqlglqosekgf 182
 QY 128 DFLPWNITLSRQKSKSINHRYQMGCE-CKITRCPMIPCVISSPDECWMWDTVEKNINGH 186

DB 183 qshlaclpreglct 199
 QY 187 QAKFFACIKRSRDGSCAW 203

RESULT 10
 ID P60275 standard; Protein; 207 AA.
 AC P60275;
 DT 08-AUG-1991 (first entry)
 DE Sequence of human natural inhibitor of collagenases (NtC).
 KW Metallo-proteinase inhibitor; wound healing; emphysema;
 FH rheumatoid arthritis therapy; ulceration; tumour metastasis.
 Key
 PT Location/qualifiers
 PR /label= signal 1..23
 PT Protein 24..207
 PR /note= "claimed"

FT Modified -site 53..55
 FT Note= "potential glycosylation site"
 FT Modified -site 101..103
 FT Note= "potential glycosylation site"
 FT EP-189784-A.
 PN 06-AUG-1986.
 PF 16-JAN-1986; 100482.
 PR 18-JAN-1985; DS-69208.
 PA (SEAR) SPARLE G D & CO.
 PI Galloway WA, Clissold PM, McCullagh KG;
 WP1; 86-205910/32.
 DR N-PSDB; N60277.
 PT New human natural inhibitor of collagenase - for treating e.g.
 PT rheumatoid arthritis or ulceration, and new DNA sequences coding
 PT for it
 PS Disclosure; Fig 2; 51pp; English.
 CC The inventors claim the AA sequence of human NIC, DNA sequences coding for
 NIC, and its RNA analogues and plasmids contg, this DNA. NIC
 CC inhibits the activity of metallo proteinases, esp. of collagenase,
 CC proteoglycanase, gelatinase or a leucocyte, macrophage or tumour
 CC cell metallo-proteinase.
 SQ Sequence 207 AA;

DB 3; Score 521; Match 41.1%; OryMatch 31.7%; Pred. No. 2.50e-44;
 Matches 81; Conservative 39; Mismatches 70; Indels 7; Gaps 7;

DB 7 lasgillllwiapsractcypphptafcnslvirakfvgtpevnqtt-lyqryeikm 65
 PR 10 LALGILLATLRLPADACSCSPVHPQQAFCNADVVTRAKAVSEKEVDSGNLDYGN-PIKR 68
 QY 66 tk-mykgfql-gdaadirfytptamesvcyfrshnrseeflqglq-dglhittc 122
 DB 123 sfrapwnsllsiaqrgrftktyvgceectvpfcslsipkglqgthclwtddqlllqgsekgf 182
 PR 128 DFTVPPWDTLSTTQKSLNHYQMGCE-CKITRCMPMPCYISSPDECILMDWTERNINGH 186
 QY 129 QSRHLACLPREPLGCTW 199

DB 183 QSRHLACLPREPLGCTW 199
 PR 187 QAKFPACIKRSQDGSACW 203

RESULT 11
 ID P60592 standard; Protein; 207 AA.
 AC P60592;
 DT 13-AUG-1991 (first entry)
 DE Sequence of a human protein having erythroid potentiating
 DE activity (EPA).
 KW Erythroid precursor growth; anaemia therapy.
 OS Homo sapiens.
 PN W08602100-A.
 PD 10-APR-1986.
 PR 01-OCT-1984; 501900.
 PR 01-OCT-1984; 501900.
 PR 01-OCT-1984; DS-656390.
 PA (SANDOZ LTD.
 PA (RECC) REGENTS OF UNIV OF CALIF.
 PI Brown E, Clark S, Golde DW, Casson JC, Hewick R, Westbrook CA;
 DR WPI; 86-106663/16.

DR N-PSDB; N60494.

PT Vectors contg. gene for protein having erythroid potentiating
 PT activity - used for producing protein to stimulate growth and
 PT formation of erythroid cells
 PS Disclosure; Fig 4; 59pp; English.
 CC The inventors claim human and gibbon EPA proteins (P60592, P60593)
 CC and cDNA that encodes EPA (N60494, N60495). The EPA protein has a
 CC biological activity of at least about 1,000,000 units per mg of
 CC protein and has an apparent molecular weight of about 28,000 daltons.
 SQ Sequence 207 AA;
 DB 3; Score 521; Match 41.1%; OryMatch 31.7%; Pred. No. 2.50e-44;
 Matches 81; Conservative 39; Mismatches 70; Indels 7; Gaps 7;
 DB 7 lasgillllwiapsractcypphptafcnslvirakfvgtpevnqtt-lyqryeikm 65
 PR 10 LALGILLATLRLPADACSCSPVHPQQAFCNADVVTRAKAVSEKEVDSGNLDYGN-PIKR 68
 QY 66 tk-mykgfql-gdaadirfytptamesvcyfrshnrseeflqglq-dglhittc 122
 DB 123 sfrapwnsllsiaqrgrftktyvgceectvpfcslsipkglqgthclwtddqlllqgsekgf 182
 PR 128 DFTVPPWDTLSTTQKSLNHYQMGCE-CKITRCMPMPCYISSPDECILMDWTERNINGH 186
 QY 129 QSRHLACLPREPLGCTW 199
 DB 183 QSRHLACLPREPLGCTW 199
 PR 187 QAKFPACIKRSQDGSACW 203

RESULT 12
 ID P60593 standard; Protein; 207 AA.
 AC P60593;
 DT 13-AUG-1991 (first entry)
 DE Sequence of a gibbon protein having erythroid potentiating
 DE activity (EPA).
 KW Erythroid precursor growth; anaemia therapy.
 OS Gibbon.
 PN W08602100-A.
 PD 10-APR-1986.
 PR 01-OCT-1984; 501900.
 PR 01-OCT-1984; DS-556590.
 PA (SANDOZ LTD.
 PA (RECC) REGENTS OF UNIV OF CALIF.
 PI Brown E, Clark S, Golde DW, Casson JC, Hewick R, Westbrook CA;
 DR WPI; 86-106663/16.

DR N-PSDB; N60494.

Db	7	laagliillwlappastractcypghptafensdliikakfvgtpevnqt-lqyryeikm	65
Qy	10	LAAGLGLATLRLPAPADACSCSPVHQAFCNADYVTRAKAVSEEVDGNDNLYGN-PIKR	68
Db	66	tk-mykgfqal-qdaadairfyypttptamesvcyfrshnrseefiagklq-dglhittc	122
Qy	69	IQEIKQIKMFKQPERDIEFITYAPSSAVCCVSLDVGGKEE-YLIAGRAEGDEKHMHTLC	127
Db	123	sfvapwnsalslaqqrgftkttyvgceectyfpc1spck1qsgsthclwtddql1qsgkfqf	182
Qy	128	DFTPVWDLTSRQKSLNHRQMGCE-CKITRCMPCTTSSPDECLMDWTEKNINGH	186
Db	183	qsrhlaclprepolctw 199	
Qy	187	QAKFACIKRSDGSCAW 203	
RESULT 13			
ID	R06749	standard; protein; 48 AA.	
AC	R06749;		
DT	16-JAN-1991	(first entry)	
DE	Peptide #1 for detection of metalloproteinases.		
KW	matrix metalloproteinase; TIMP-2 (CSC-21K).		
OS	Synthetic.		
PN	US7494796-A.		
PD	21-AUG-1990.		
PF	13-MAR-1990;	494796.	
PR	21-MAR-1989;	US-326334.	
PPR	17-JUL-1989;	US-380431.	
PR	18-AUG-1989;	US-395453.	
PR	13-MAR-1990;	US-494796.	
PA	(USSH) NAT INST OF HEALTH.		
PI	Steiler-Sevenson WG, Liotta LA, Krutzsch HC;		
WPI	90-290097/38		
DR	New matrix metallo-proteinase inhibitor - used to treat diseases		
PT	resulting from matrix metallo-proteinase activity and in		
PT	diagnosis, detection and purification..		
PT	Example: Page 37, 54pp; English.		
PS	One of three peptides lacking cysteine or having only one cysteine		
CC	which were found to be useful for detecting metalloproteinases in		
CC	animal and human tissues or in body fluids which may have		
CC	antibodies to the protein. The peptides can also be used to elicit		
CC	antibodies for use in detecting metalloproteinases.		
CC	See also Q05937, R06746-R06748, R06694-R06895 and		
CC	Q05938-05940.		
Sequence 48 AA;			

Reaction	Time (min)	Conc. (M)	Conc. (M)
Db	1	diygnpikriyekqikfkqiekdiefitytapsassavqeyldvggk	48
QV	60	DIYGNPIRKIQYEKQIKNFKGKEDIEFITYTAPSSACVGSDVGGK	107

RESULT 14
 ID R47010 standard; Protein; 28 AA.
 AC R47010;
 16-MET-1994 (First entry)
 16-MET-1994 inhibitor 2 position 187-214.
 DE DE

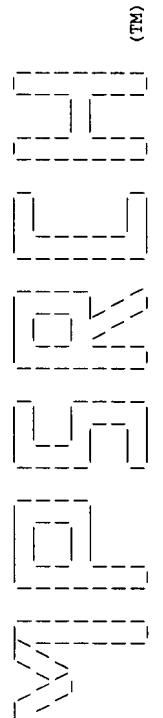
KW	Naturally-occurring immunomodulatory protein; human; therapy; class major histocompatibility complex; class II; allotropy; type I diabetes; autoimmune disease; rheumatoid arthritis; T-cell-mediated response; multiple sclerosis; transplant rejection; vaccine; MHC.
HomO	Homo sapiens.
OS	OS
PN	PN
W09404171-A.	PD 03-MAR-1994.
PF	PF 11-AUG-1993; 007545.
PR	PR 11-AUG-1992; US-925460.
PR	PR 15-JUN-1993; US-925460.
PA	PA (HARD) HARVARD COLLEGE.
PI	PI Chicz RM, Hedley MI, Stern LJ, Strominger JL, Urban RG;
PI	PI Vignal Dr;
WPI	WPI; 94-0822825/10.
DR	DR Novel immunomodulatory peptide(s) and nucleic acids - useful for treatment of auto:immune diseases, transplant rejection and for vaccination
PT	PT Disclosure; Page 48; 139pp; English.
PS	PS The sequences given in R49291-505 and R46981-7038 represent peptide fragments of naturally-occurring immunomodulatory proteins. These fragments are between 10-30 residues in length and bind to a human major histocompatibility complex (MHC) class II allotype. These peptides may be used for therapy of autoimmune diseases, such as type I diabetes, rheumatoid arthritis and multiple sclerosis, and to reduce transplant rejection. They may also be used for vaccination providing an exclusively T-cell-mediated response, which can be class I or class-II based, or both, depending on the length and character of the immunogenic peptides.
Sequence	Sequence 28 AA;
DB 9;	Score 219; Match 100.0%; QryMatch 13.3%; Pred. No. 4-12e-15
Matches	Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	Db 1 qakffacikrksdsgcawrygaappkqef 28 1 1 1 1 1 1 1 187 QAKFFACIKRKS DSGCAWRYGAAPPKQEF 214
Qy	Qy
RESULT	RESULT 15
ID	ID R06894 standard; protein; 24 AA.
R06894;	R06894; 16-JAN-1991 (first entry)
AC	AC DT Peptide #3 for detection of metalloproteinas.
AC	AC DE matrix metalloproteinase; TIMP-2 (CSC-21K).
AC	AC KW Synthetic.
OS	OS US7494796-A.
OS	OS 21-AUG-1990.
PN	PN 21-MAR-1989; US322334.
PN	PN 13-MAR-1980; 494796.
PR	PR

12 JUL 1989, US-380431.
 PR 17-JUL-1989; US-380431.
 PR 18-AUG-1989; US-393453.
 PR 13-MAR-1990; US-494796.
 PA (USSR) NAT INST OF HEALTH.
 Stetler-Sevenson WG, Liotta LA, Krutzsch HC;
 PI WP; 90-29009/38.
 DR PT
 PT
 PT
 PT
 PS Page 37; 54pp; English.
 CCC Example of three peptides lacking cysteine or having only one cysteine

CC which were found to be useful for detecting metalloproteinases in animal and human tissues or in body fluids which may have CC antibodies to the protein. The peptides can also be used to elicit CC antibodies for use in detecting metalloproteinases. CC See also Q05937, R06746-R06750, R06895 and Q05538-Q05940. SQ Sequence 24 AA;

DB 2; Score 170; Match 100.0%; QryMatch 10.3%; Pred. No. 3.05e-07; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2 hitlccdfivpwtl1stqkksln 24
 Qy 123 HITLCDFIVPWTL1STQKKSLN 145
 Search completed: Mon Feb 5 16:59:06 1996
 Job time : 26 secs.



Release 2.1D John F. Collins, Biocomputing Research Unit, 1993, University of Edinburgh, U.K.
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MSrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Feb 5 17:01:32 1996; MacPar time 2.09 Seconds
 194.539 Million cell updates/sec
 Tabular output not generated.

Title: >FIG2
 Perfect Score: 1643
 Sequence: 1 MGAAARTLRLAIGLILATL.....CAWYRGAAPQOEFLIEDP 220

Scoring table: PAM 150
 Gap 11

Searched: 19663 seqs, 1851369 residues
 Database: a-issued
 1 51
 2 52
 3 53
 4 54
 5 PCT90
 6 PCT91
 7 PCT92
 8 PCT93
 9 PCT94
 10 PCT95

Statistics: Mean 30.075; Variance 124.991; scale 0.241
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	219	13.3	28	8 PCT-US93-0	Sequence 245, Application 1.40e-11	
2	157	9.6	19	8 PCT-US93-0	Sequence 246, Application 5.57e-06	
3	91	5.5	3033	4 US-07-925-	Sequence 9, Application 1.68e+00	
4	91	5.5	3033	4 US-07-925-	Sequence 8, Application 1.68e+00	
5	79	4.8	990	10 PCT-US94-0	Sequence 2, Application 1.32e+01	
6	79	4.8	476	9 PCT-US94-0	Sequence 12, Application 1.32e+01	
7	79	4.8	397	10 PCT-US95-0	Sequence 14, Application 1.32e+01	
8	75	4.6	928	9 PCT-US94-1	Sequence 3, Application 2.55e+01	
9	75	4.6	928	9 PCT-US94-1	Sequence 2, Application 2.55e+01	
10	74	4.5	490	10 PCT-US95-0	Sequence 13, Application 3.00e+01	
11	74	4.5	778	8 PCT-US93-0	Sequence 4, Application 3.00e+01	
12	74	4.5	480	4 US-07-803-	Sequence 2, Application 3.00e+01	
13	73	4.4	883	3 US-08-106-	Sequence 8, Application 4.86e+01	
14	71	4.3	659	10 PCT-US93-0	Sequence 1, Application 5.70e+01	
15	70	4.3	239	8 PCT-US93-0	Sequence 2, Application 5.70e+01	
16	70	4.3	2446	8 PCT-US93-1	Sequence 2, Application 5.70e+01	
17	70	4.3	1513	8 PCT-US93-0	Sequence 3, Application 5.70e+01	
18	70	4.3	778	8 PCT-US93-0	Sequence 3, Application 5.70e+01	
19	70	4.3	112	8 PCT-US93-0	Sequence 8, Application 6.67e+01	
20	69	4.2	104	3 US-07-789-	Sequence 12, Application 6.67e+01	
21	69	4.2	180	4 US-07-953-	Sequence 65, Application 6.67e+01	
22	69	4.2	286	8 PCT-US93-0	Sequence 2, Application 6.67e+01	
23	69	4.2	336	7 PCT-US92-1	Sequence 2, Application 6.67e+01	
24	68	4.1	474	10 PCT-US95-0	Sequence 5, Application 7.80e+01	
25	68	4.1	434	2 US-07-679-	Sequence 15, Application 7.80e+01	
26	68	4.1	567	4 US-08-001-	Sequence 2, Application 7.80e+01	
27	68	4.1	214	4 US-07-953-	Sequence 11, Application 7.80e+01	
28	68	4.1	575	3 US-07-683-	Sequence 2, Application 7.80e+01	
29	67	4.1	3011	9 PCT-US91-0	Sequence 1, Application 9.12e+01	
30	67	4.1	364	8 PCT-US93-1	Sequence 15, Application 9.12e+01	
31	67	4.1	3033	4 US-07-925-	Sequence 5, Application 9.12e+01	
32	67	4.1	3011	8 PCT-US93-0	Sequence 1, Application 9.12e+01	
33	67	4.1	477	3 US-07-847-	Sequence 2, Application 1.06e+02	
34	67	4.1	66	4 US-08-186-	Sequence 2, Application 1.06e+02	
35	67	4.1	355	6 PCT-US94-0	Sequence 2, Application 1.06e+02	
36	67	4.1	782	4 US-08-100-	Sequence 15, Application 1.06e+02	
37	67	4.1	364	8 PCT-US93-1	Sequence 9, Application 1.06e+02	
38	66	4.0	21	2 US-07-679-	Sequence 2, Application 1.06e+02	
39	66	4.0	477	3 US-07-847-	Sequence 9, Application 1.06e+02	
40	66	4.0	481	4 US-08-186-	Sequence 2, Application 1.06e+02	
41	66	4.0	481	9 PCT-US94-0	Sequence 2, Application 1.06e+02	
42	66	4.0	1167	3 PCT-US95-0	Sequence 187, Application 1.06e+02	
43	66	4.0	18	10 PCT-US95-0	Sequence 30, Application 1.06e+02	
44	66	4.0	29	9 PCT-US95-0	Sequence 98, Application 1.06e+02	
45	66	4.0	481	10 PCT-US95-0	Sequence 98, Application 1.06e+02	

ALIGNMENTS

Db	1	QAKFFACIKRSQGSCAWYR 19		
Qy	187	QAKFFACIKRSQGSCAWYR 205		
RESULT 3				
ID	US-07-925-695-9	STANDARD;	PRT;	3033 AA.
XX	XX	DE	Sequence 9, Application US/07925695.	
AC	XX	XX	Sequence 9, Application US/07925695.	
XXXXXX	XX	XX	GENERAL INFORMATION:	
CC	AC	AC	APPLICANT: OKAMOTO, Hiroaki	
CC	XX	XX	APPLICANT: NAKAMURA, Tetsuo	
CC	DT	01-JAN-1900	TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOME,	
CC	CC	CC	TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, ANTIGEN, ANTIBODY	
CC	CC	CC	TITLE OF INVENTION: DETECTION SYSTEMS	
CC	CC	CC	NUMBER OF SEQUENCES: 9	
CC	CC	CC	CORRESPONDENCE ADDRESS:	
CC	CC	CC	ADDRESSEE: Beveridge, DeGrandi, Weilacher & Young	
CC	CC	CC	STREET: 1850 M Street, N.W., Suite 800	
CC	CC	CC	CITY: Washington	
CC	CC	CC	STATE: D.C.	
CC	CC	CC	COUNTRY: US	
CC	CC	CC	ZIP: 20036	
CC	CC	CC	COMPUTER READABLE FORM:	
CC	CC	CC	MEDIUM TYPE: Floppy disk	
CC	CC	CC	COMPUTER: IBM PC compatible	
CC	CC	CC	OPERATING SYSTEM: PC-DOS/MS-DOS	
CC	CC	CC	SOFTWARE: Patent In Release #1.0, Version #1.25	
CC	CC	CC	CURRENT APPLICATION DATA:	
CC	CC	CC	APPLICATION NUMBER: US/07/925,695	
CC	CC	CC	FILING DATE: 1992/08/07	
CC	CC	CC	CLASSIFICATION: 435	
CC	CC	CC	PRIOR APPLICATION DATA:	
CC	CC	CC	APPLICATION NUMBER: JP 287402/91	
CC	CC	CC	FILING DATE: 09-AUG-1991	
CC	CC	CC	PRIOR APPLICATION DATA:	
CC	CC	CC	APPLICATION NUMBER: JP 360441/91	
CC	CC	CC	FILING DATE: 05-DEC-1991	
CC	CC	CC	ATTORNEY/AGENT INFORMATION:	
CC	CC	CC	NAME: Weilacher, Robert G.	
CC	CC	CC	REGISTRATION NUMBER: 20 531	
CC	CC	CC	REFERENCE/DOCKET NUMBER: 06/87-48009	
CC	CC	CC	TELECOMMUNICATION INFORMATION:	
CC	CC	CC	TELEPHONE: (202) 659-2811	
CC	CC	CC	TELEFAX: (202) 659-1462	
CC	CC	CC	TELEX: WU 64470	
CC	CC	CC	SEQUENCE CHARACTERISTICS:	
CC	CC	CC	LENGTH: 3033 amino acids	
CC	CC	CC	TYPE: AMINO ACID	
CC	CC	CC	STRANDEDNESS: unknown	
CC	CC	CC	TOPOLOGY: linear	
CC	CC	CC	SEQUENCE: 3033 AA: 330352 MW: 48662901 CN:	

DB 4; Score 91; Match 25.5%; QryMatch 5.5%; Pred. No. 1.68e+00; 5;
 Matches 24; Conservative 27; Mismatches 37; Indels 6; Gaps 5;
 Db 2739 IKALAACGAAAGIVDPVMLVCGDDLVVILSEQNEEDRNLRAFTEAMTR--YSAPPDLP 2796
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 Qy 21 LRPADACSCSP-VHPQAFCNADVVAKAYSEKEVTSQGNDIYGNPPIKRIQEIKQIKMF 79
 Db 2797 R-PYEDELEI-TSCSSNN-SYALDSRERRYFIL 2827
 Db ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:::
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RESULT 4
 ID US-07-925-695-8 STANDARD; PRT; 3033 AA.
 XX
 AC
 XXXXXX
 XX DT 01-JAN-1900
 DE Sequence 8, Application US/07925695.
 XX
 CC Sequence 8, Application US/07925695
 GENERAL INFORMATION:
 APPLICANT: OKAMOTO, Hiroaki
 APPLICANT: NAKAMURA, Tetsuo
 TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOME,
 TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, ANTIGEN, ANTIBOD
 AND
 TITLE OF INVENTION: DETECTION SYSTEMS
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Beveridge, Degrandi, Weilacher & Young
 STREET: 1850 M Street, N.W., Suite 800
 CITY: Washington
 STATE: D.C.
 COUNTRY: US
 ZIP: 20036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/925,695
 FILING DATE: 19920807
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 287402/91
 FILING DATE: 09-AUG-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 360441/91
 FILING DATE: 05-DEC-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Weilacher, Robert G.
 REGISTRATION NUMBER: 20,331
 REFERENCE/DOCKET NUMBER: 06/87-48009
 TELECOMMUNICATION INFORMATION:
 TELEFAX: (202) 659-2811
 CC TELEFAX: (202) 659-1462

CC TELEPHONE: 201-831-3244
 CC TELEX/FAX: 201-831-3305
 CC INFORMATION FOR SEQ ID NO: 2:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 990 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQUENCE: 990 AA; 111713 MW; 5013050 CN;
 SQ DB 10; Score 79; Match 32.1%; QryMatch 4.8%; Pred. No. 1.32e+01; Gaps 2;
 Matches 17; Conservative 12; Mismatches 22; Indels 2; Gaps 2;
 DE Db 273 GV-FSFGTOKALDDAMLRDVGKTLQTAIYLRS-DSLSATDRKCKLERYLLG 323
 AC Qy 99 GVSIDVGKKEYLIAAGKAEGDGKMHITLCDFIVPWDLISITQKKSILNHRYQMG 151.
 RESULT 6
 ID ID PCT-US94-06430-12 STANDARD; PRT; 476 AA.
 XX DE Sequence 12, Application PC/TUS9406430.
 XX CC Sequence 12, Application PC/TUS9406430
 CC GENERAL INFORMATION:
 CC APPLICANT: The Upjohn Company
 CC TITLE OF INVENTION: Lettuce Infectious Yellows Virus Genes
 CC NUMBER OF SEQUENCES: 25
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: The Upjohn Company, Corp. Intellectual
 CC STREET: 301 Henrietta Street
 CC CITY: Kalamazoo
 CC STATE: Michigan
 CC COUNTRY: USA
 CC ZIP: 49001
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: PatentIn Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US94/06430
 CC FILING DATE:
 CC CLASSIFICATION:
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Darnley Jr., James D.
 CC REGISTRATION NUMBER: 33,673
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 616-385-5210
 CC TELEX: 224401
 CC INFORMATION FOR SEQ ID NO: 12:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 476 amino acids
 CC TYPE: amino acid

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CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 397 AA; 43552 MW; 781935 CN;
DB 10; Score 79; Match 26.1%; OryMatch 4.8%; Pred. No. 1.32e+01;
Matches 12; Conservative 13; Mismatches 19; Indels 2; Gaps 2;
Qy 47 AKAVSEKE-VDSGNDIVCNP-TKRIQEIKQIKMFKGPKEDIEFY 90

RESULT 8
ID PCT-US94-10357-3 STANDARD; PRT; 928 AA.
XX
AC xxxxx
XX
DT 01-JAN-1990
XX
DE Sequence 3, Application PC/TUSS9410357.
XX
CC Sequence 3, Application PC/TUSS9410357
GENERAL INFORMATION:
CC APPLICANT: The Regents of the University of California
CC APPLICANT: and Canju, Inc.
CC TITLE OF INVENTION: Therapeutic Use of the Retinoblastoma
CC TITLE OF INVENTION: Susceptibility Gene Product
CC NUMBER OF SEQUENCE: 3
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Campbell and Flores
CC STREET: 4370 La Jolla Village Drive
CC CITY: San Diego
CC STATE: California
CC COUNTRY: USA
CC ZIP: 92122
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US94/10357
CC FILING DATE: 13-SEP-1994
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/121,108
CC FILING DATE: 13-SEP-1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Campbell,1, Kathryn A.
CC REGISTRATION NUMBER: 31 814.5
CC REFERENCE/DOCKET NUMBER: FP-UC 1117
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (619) 535-9001
CC TELEFAX: (619) 535-8949
CC INFORMATION FOR SEQ ID NO: 3:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 928 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear

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SQ SEQUENCE 928 AA; 106061 MW; 4602767 CN;

DB 9; Score 75; Match 31.3%; QryMatch 4.6%; Pred. No. 2.55e+01; Indels 5; Gaps 4;

Matches 15; Conservative 15; Mismatches 13; Indels 5; Gaps 4;

- Db 136 KEIDTSKTV-DNAMSRLKRYDV-LFALFSKLERTELYLTQPSSSI 181

Qy 53 KEVDSSNDIYGNPIKRI--QYEIKQIRMFKGPEKIDFY-TAPSSAV 97

RESULT 10 ID PCT-US95-05744-13 STANDARD; PRT; 490 AA.

9 ID PCT-US94-10357-2 STANDARD; PRT; 928 AA.

XX AC xxxxxx

XX DT 01-JAN-1900

XX DE Sequence 2, Application PC/TUS9410357.

XX CC Sequence 2, Application PC/TUS9410357

CC CC GENERAL INFORMATION:

CC CC APPLICANT: The Regents of the University of California

CC CC APPLICANT: and Canji, Inc.

CC CC TITLE OF INVENTION: Therapeutic Use of the Retinoblastoma

CC CC TITLE OF INVENTION: Susceptibility Gene Product

CC CC NUMBER OF SEQUENCES: 3

CC CC CORRESPONDENCE ADDRESS:

CC CC ADDRESSEE: Campbell and Flores

CC CC STREET: 4370 La Jolla Village Drive

CC CC CITY: San Diego

CC CC STATE: California

CC CC COUNTRY: USA

CC CC ZIP: 92112

CC CC COMPUTER READABLE FORM:

CC CC MEDIUM TYPE: Floppy disk

CC CC COMPUTER: IBM PC compatible

CC CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC CC SOFTWARE: PatentIn Release #1.0, Version #1.25

CC CC CURRENT APPLICATION DATA:

CC CC APPLICATION NUMBER: PCT/US94/10357

CC CC FILING DATE: 13-SEP-1994

CC CC CLASSIFICATION:

CC CC PRIOR APPLICATION DATA:

CC CC APPLICATION NUMBER: US 08/121,108

CC CC FILING DATE: 13-SEP-1993

CC CC ATTORNEY/AGENT INFORMATION:

CC CC NAME: Campbell, Kathryn A.

CC CC REGISTRATION NUMBER: 31,815

CC CC REFERENCE/DOCKET NUMBER: FP-UC 11117

CC CC TELEPHONE: (619) 535-8949

CC CC INFORMATION FOR SEQ ID NO: 2:

CC CC SEQUENCE CHARACTERISTICS:

CC CC LENGTH: 928 amino acids

CC CC TYPE: amino acid

CC CC TOPOLOGY: linear

CC CC MOLECULE TYPE: protein

SQ SEQUENCE 928 AA; 106144 MW; 4604196 CN;

DB 9; Score 75; Match 31.3%; QryMatch 4.6%; Pred. No. 2.55e+01; Indels 5; Gaps 4;

Matches 15; Conservative 15; Mismatches 13; Indels 5; Gaps 4;

- Db 136 KEIDTSKTV-DNAMSRLKRYDV-LFALFSKLERTELYLTQPSSSI 181

Qy 53 KEVDSSNDIYGNPIKRI--QYEIKQIRMFKGPEKIDFY-TAPSSAV 97

RESULT 10 ID PCT-US95-05744-13 STANDARD; PRT; 490 AA.

9 ID PCT-US94-10357-2 STANDARD; PRT; 928 AA.

XX AC xxxxxx

XX DT 01-JAN-1900

XX DE Sequence 13, Application PC/TUS9505744.

CC CC GENERAL INFORMATION:

CC CC APPLICANT: GOLDSTEIN, Joyce A.

CC CC APPLICANT: ROMGES-SPARKS, Marjorie

CC CC APPLICANT: DE MORAIS, Sonia M.F.

CC CC TITLE OF INVENTION: CLONING, EXPRESSION AND DIAGNOSIS OF HUMAN

CC CC TITLE OF INVENTION: CYTOCHROME P450 2C19: THE PRINCIPAL DETERMINANT

CC CC TITLE OF INVENTION: OF S-MEPHENYTOIN METABOLISM

CC CC NUMBER OF SEQUENCES: 61

CC CC CORRESPONDENCE ADDRESS:

CC CC ADDRESSEE: Townsend and Townsend Khourie and Crew

CC CC STREET: 319 Lytton Avenue

CC CC CITY: Palo Alto

CC CC STATE: California

CC CC COUNTRY: US

CC CC ZIP: 94301

CC CC COMPUTER READABLE FORM:

CC CC MEDIUM TYPE: Floppy disk

CC CC COMPUTER: IBM PC compatible

CC CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC CC SOFTWARE: PatentIn Release #1.0, Version #1.25

CC CC CURRENT APPLICATION DATA:

CC CC APPLICATION NUMBER: PCT/US95/05744

CC CC FILING DATE:

CC CC CLASSIFICATION:

CC CC PRIOR APPLICATION DATA:

CC CC APPLICATION NUMBER: US 08/238,821

CC CC FILING DATE: 06-MAY-1994

CC CC PRIOR APPLICATION DATA:

CC CC APPLICATION NUMBER: 08/201,118

CC CC FILING DATE: 22-FEB-1994

CC CC PRIOR APPLICATION DATA:

CC CC APPLICATION NUMBER: US 07/864,962

CC CC FILING DATE: 09-APR-1992

CC CC ATTORNEY/AGENT INFORMATION:

CC CC NAME: Dow, Karen B.

CC CC REGISTRATION NUMBER: 29,684

CC CC REFERENCE/DOCKET NUMBER: 15280-192-1-1

CC CC TELECOMMUNICATION INFORMATION:

CC CC TELEPHONE: (415) 326-2400

CC CC TELEFAX: (415) 326-2422

CC CC INFORMATION FOR SEQ ID NO: 13:

CC CC SEQUENCE CHARACTERISTICS:

LENGTH: 778 amino acids
 TYPE: AMINO ACID
 TOPOLogy: linear
 MOLECULE TYPE: protein
 SEQUENCE 778 AA: 8'981 MW: 3142889 CN:
 DB 8; Score 74; Match 24.3%; QryMatch 4.5%; Pred. No. 3.00e+01; Gaps 4;
 Matches 17; Conservative 12; Mismatches 37; Index 4;
 DDb 159 KHHFVYH-PIKEETCSCPACYDAKIHLISSRFIRPSDRNQKNSISDPNIDRINLVLG 217
 QY 84 KDFELITVATPSSAVCGSYSLD-VGGKEYLLAGK-AEGDGRMHI-TLCDFTPWNTLSTIQ 140
 DDb 218 KQALPESWPM 227
 QY 141 KKSЛИНHYQМ 150
 RESULT 12
 ID US-07-803-636A-2
 STANDARD;
 PRT; 480 AA.
 XXXXXXXX
 01-JAN-1900
 Sequence 2, Application US/07803636A.
 Sequence 2, Application US/07803636A
 GENERAL INFORMATION:
 APPLICANT: MCGLWAIN, TERRY F. MCGLWAIN, LANCE E. PERRYMAN
 APPLICANT: MCGLWAIN, TERRY F. MCGLWAIN, LANCE E. PERRYMAN
 APPLICANT: WILLIAM C. DAVIS
 APPLICANT: WILLIAM C. DAVIS
 TITLE OF INVENTION: IMMUNIZATION AGAINST BABESIOSIS USING
 TITLE OF INVENTION: IMMUNIZATION AGAINST BABESIOSIS USING
 SIMILAR
 TITLE OF INVENTION: IMMUNOGENS
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DAVID R. SALIWANCHIK
 STREET: 2421 NW 41ST STREET, SUITE A-1
 CITY: GAINESVILLE
 STATE: FLORIDA
 COUNTRY: USA
 ZIP: 32606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/803, 636A
 FILING DATE: 19911206
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: SALIWANCHIK, DAVID R.
 REGISTRATION NUMBER: 311794
 REFERENCED DOCKET NUMBER: WA4-059 .C1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 904-375-8100
 TELEFAX: 904-372-5800
 INFORMATION FOR SEQ ID NO: 2;

LENGTH: 883 Amino Acids
 TYPE: Amino Acids
 STRANDEDNESS: Not applicable
 TOPOLOGY: Not applicable
 MOLECULE TYPE: protein
 HYPOTHETICAL: No
 ANTI-SENSE: No
 FRAGMENT TYPE: Entire protein
 ORIGINAL SOURCE:
 ORGANISM: Bacteriophage T7
 STRAIN: Not applicable
 INDIVIDUAL ISOLATE: Not applicable
 DEVELOPMENTAL STAGE: Not applicable
 HAPLOTYPE: Not applicable
 TISSUE TYPE: Not applicable
 CELL TYPE: Not applicable
 ORGANELLE: Not applicable
 IMMEDIATE SOURCE:
 LIBRARY: Not applicable
 CLONE: PKGP-HA1mut4
 POSITION IN GENOME:
 CHROMOSOME SEGMENT: Not applicable
 MAP POSITION: Not applicable
 UNITS: Not applicable
 FEATURE:
 NAME/KEY: T7 RNA Polymerase GP1(lys2)
 LOCATION: 1 to 883
 IDENTIFICATION METHOD: By expressing the protein
 IDENTIFICATION METHOD: The protein sequence
 OTHER INFORMATION: The glut 1 to lys 883
 OTHER INFORMATION: residue 222 altered
 OTHER INFORMATION: T7 RNA polymerase
 PUBLICATION INFORMATION:
 AUTHORS: Ikeda, R.A., Chang, L.I., a
 TITLE: Selection and Characterization
 TITLE: of RNA Polymerase That Recognizes
 TITLE: of T7-like Promoters
 JOURNAL: Biochemistry
 VOLUME: 32
 ISSUE: 35
 PAGES: 9115-9124
 DATE: Sept. 7, 1993
 DOCUMENT NUMBER:
 FILING DATE:
 PUBLICATION DATE:
 RELEVANT RESIDUES IN SEQ ID NO: Amin
 RELEVANT RESIDUES IN SEQ ID NO: 883
 rase
 CC RELEVANT RESIDUES IN SEQ ID NO: GP1(lys2)
 CC RELEVANT RESIDUES IN SEQ ID NO: GP1(lys2)
 CC RELEVANT RESIDUES IN SEQ ID NO: Glu
 CC RELEVANT RESIDUES IN SEQ ID NO:
 SQ SEQUENCE 883 AA; 98854 MW; 389993 CN;
 DB 3; Score 73; Match 27.5%; OryMatch
 Matches 11; Conservative 13; Mismatches
 222.
 556 GRAVNLLPSETVQDYGIVAKKVN-EILLOADINGTN
 DB

Qy 47 AKAVSEKEVDGNDIYGNPIKRYOYEIKQIRMFKGPKPKDI 86

RESULT 14 ID PCT-US95-05008-8 STANDARD; PRT; 659 AA.

XX AC XXXXX

XX DT 01-JAN-1900

DE Sequence 8, Application PC/TUS9505008.

XX Sequence 8, Application PC/TUS9505008

CC GENERAL INFORMATION:

CC APPLICANT: Sugen, Inc.

CC APPLICANT: 515 Galveston Drive

CC Redwood City, California 94063-4720

CC APPLICANT: United States of America

CC Wissenschaften E.V.

CC APPLICANT: Hotgarten Str. 2

CC APPLICANT: München 80539

CC APPLICANT: Germany

CC TITLE OF INVENTION: Novel Megakaryocytic Protein Tyrosine

CC NUMBER OF SEQUENCES: 21

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Pennie & Edmonds

CC STREET: 1155 Avenue of the Americas

CC CITY: New York

CC STATE: New York

CC COUNTRY: U.S.A.

CC ZIP: 10036

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: Patent Release #1.0, version #1.25

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: PCT/US95/05008

CC FILING DATE: 24-APR-1995

CC CLASSIFICATION:

CC PRIORITY APPLICATION DATA:

CC APPLICATION NUMBER: US 08/232,545

CC FILING DATE: 22-APR-1994

CC CLASSIFICATION:

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Coruzzi, Laura A.

CC REGISTRATION NUMBER: 30,742

CC REFERENCE/DOCKET NUMBER: 768-3-074

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: (212)790-9090

CC TELEFAX: (212)869-9741

CC INFORMATION FOR SEQ ID NO: 8:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 659 amino acids

CC TYPE: amino acid

CC STRANDEDNESS: unknown

CC TOPOLOGY: unknown

CC MOLECULE TYPE: protein

CC SEQUENCE 659 AA; 76281 MW; 2353510 CN;

DB 10; Score 71; Match 47.8%; QryMatch 4.3%; Pred. No. 4.86e+01; Index 2; Gaps 2;

Matches 11; Conservative 5; Mismatches 5;

Db 422 RGGYDV-AIKMKEGMSDFI 443

Qy 68 RIYEITQIKRPF-GPEKDI 89

RESULT 15

ID PCT-US93-01652-1 STANDARD; PRT; 239 AA.

XX

AC XXXXX

XX DT 01-JAN-1900

XX Sequence 1, Application PC/TUS9301652.

CC GENERAL INFORMATION:

CC APPLICANT: Bouch, Noel P.

CC APPLICANT: Polverini, Peter J.

CC APPLICANT: Good, Deborah J.

CC APPLICANT: Frazier, William A.

CC TITLE OF INVENTION: Method and Composition for

CC INHIBITING Angiogenesis

CC NUMBER OF SEQUENCES: 12

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Tilton Fallon, Lungmus & Chestnut

CC STREET: 100 South Wacker Drive, Suite 960

CC CITY: Chicago

CC STATE: Illinois

CC COUNTRY: USA

CC ZIP: 60606-4002

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: Patent Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: PCT/DS93/01652

CC FILING DATE: 24-FEB-1992

CC PRIORITY APPLICATION DATA:

CC APPLICATION NUMBER: US/07/841,656

CC PRIORITY APPLICATION DATA:

CC APPLICATION NUMBER: US/07/464,369

CC FILING DATE: 12-JAN-1990

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Fenstress, Susan B.

CC REGISTRATION NUMBER: 31,327

CC REFERENCE/DOCKET NUMBER: 92005-PCT

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: (312)-456-8000

CC TELEFAX: (312)-456-7776

CC INFORMATION FOR SEQ ID NO: 1:

CC SEQUENCE CHARACTERISTICS:

11.1	0771	12	0772	13	0781	14	0782	15	0791	16	0792	17	0800	18	0801	19	0802	20	0803	21	0804	22	0805	23	0806	24	0807	25	0808	26	0809	27	0810	28	0811	29	0812	30	0813	31	0814	32	0815	33	0816	34	0817	35	0818	36	0819	37	0820	38	0821	39	0822	40	0823	41	0824	42	0825	43	0826	44	0827	45	0828	46	0829	47	0830	48	0831	49	0832	50	0833	51	0834	52	0835	53	0836	54	0837	55	0838	56	0839	57	0840	58	0841	59	0842	60	0843	61	0844	62	0845	63	0846	64	0847	65	0848	66	0849	67	0850	68	0851	69	0852
------	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------	----	------

Statistics: Mean 30.214; Variance 114.839; scale 0.263

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	1643	100.0	220	33	US-08-167- Sequence 10, Applicati	1.12e-168
2	1607	97.8	220	33	US-08-167- Sequence 11, Applicati	1.24e-164
3	1550	94.3	220	33	US-08-167- Sequence 12, Applicati	3.14e-158
4	844	51.4	224	4	PCT-US94-1 Sequence 2, Applicatio	2.19e-79
5	695	42.3	211	4	PCT-US94-1 Sequence 13, Applicati	6.06e-63
6	695	42.3	211	30	US-08-134- Sequence 13, Applicati	6.06e-63
7	695	42.3	211	4	PCT-US94-1 Sequence 2, Applicatio	6.06e-63
8	695	42.3	211	48	US-08-134- Sequence 2, Applicatio	6.06e-63
9	686	41.8	212	33	US-08-167- Sequence 13, Applicati	5.91e-62
10	686	41.8	211	33	US-08-167- Sequence 14, Applicati	5.91e-62
11	685	41.7	198	30	US-08-134- Sequence 15, Applicati	7.61e-62
12	685	41.7	198	4	PCT-US94-1 Sequence 15, Applicati	7.61e-62
13	673	41.0	188	33	US-08-167- Sequence 1, Applicatio	1.58e-60
14	556	33.8	164	30	US-08-134- Sequence 17, Applicati	9.90e-48
15	556	33.8	164	4	PCT-US94-1 Sequence 17, Applicati	9.90e-48
16	521	31.7	207	33	US-08-167- Sequence 6, Applicatio	6.31e-44
17	518	31.5	206	33	US-08-167- Sequence 7, Applicatio	1.33e-43
18	517	31.5	207	33	US-08-167- Sequence 4, Applicatio	1.71e-43
19	506	30.8	205	33	US-08-167- Sequence 8, Applicatio	2.67e-42
20	488	29.7	209	33	US-08-167- Sequence 9, Applicatio	2.37e-40
21	476	29.0	207	33	US-08-167- Sequence 5, Applicatio	4.69e-39
22	470	28.6	125	33	US-08-167- Sequence 16, Applicati	2.08e-38
23	219	13.3	28	65	US-08-167- Sequence 245, Applicat	5.29e-12
24	219	13.3	28	65	US-08-488- Sequence 245, Applicat	5.29e-12
25	219	13.3	28	24	US-08-077- Sequence 245, Applicat	5.29e-12
26	219	13.3	28	24	US-08-077- Sequence 245, Applicat	5.29e-12
27	219	13.3	28	65	US-08-488- Sequence 245, Applicat	5.29e-12
28	219	13.3	28	64	US-08-476- Sequence 245, Applicat	5.29e-12
29	219	13.3	28	65	US-08-480- Sequence 245, Applicat	5.29e-12
30	219	13.3	28	64	US-08-475- Sequence 245, Applicat	5.29e-12
31	157	9.6	19	65	US-08-488- Sequence 246, Applicat	6.71e-06
32	157	9.6	19	65	US-08-488- Sequence 246, Applicat	6.71e-06
33	157	9.6	19	64	US-08-475- Sequence 246, Applicat	6.71e-06
34	157	9.6	19	64	US-08-476- Sequence 246, Applicat	6.71e-06
35	157	9.6	19	65	US-08-480- Sequence 246, Applicat	6.71e-06
36	157	9.6	19	65	US-08-487- Sequence 246, Applicat	6.71e-06
37	157	9.6	19	24	US-08-077- Sequence 246, Applicat	6.71e-06
38	157	9.6	19	24	US-08-077- Sequence 2, Applicatio	4.16e-04
39	138	8.4	25	64	US-08-474- Sequence 21, Applicati	1.85e-03
40	131	8.0	18	33	US-08-167- Sequence 18, Applicati	3.45e-02
41	117	7.1	18	33	US-08-167- Sequence 19, Applicati	4.24e-02
42	116	7.1	18	33	US-08-167- Sequence 20, Applicati	1.06e-01
43	100	6.1	28	31	US-08-141- Sequence 1, Applicatio	1.29e-00
44	99	6.0	18	33	US-08-167- Sequence 4, Applicatio	2.32e+00
45	96	5.8	76	67	US-08-538- Sequence 1, Applicati	2.20e+00

ALIGNMENTS

RESULT 1	XX	Sequence 10, Application US/08167463.
ID	XX	GENERAL INFORMATION:
XX	XX	APPLICANT: HAWKES, SUSAN P.
AC	XX	APPLICANT: KISHORANI, NARENDRAS.
XXXX	XX	APPLICANT: YANG, TE-YUAN
DT	01-JAN-1900	TITLE OF INVENTION: HUMAN TIMP-3
XX	XX	NUMBER OF SEQUENCES: 32
DE	XX	CORRESPONDENCE ADDRESS:
XX	XX	ADDRESSEE: MORRISON & FOERSTER
XX	XX	STREET: 755 Page Mill Road
XX	XX	CITY: Palo Alto
XX	XX	STATE: California
XX	XX	COUNTRY: USA
XX	XX	ZIP: 94304-1018
XX	XX	COMPUTER READABLE FORM:
XX	XX	MEDIUM TYPE: Floppy disk
XX	XX	COMPUTER: IBM PC compatible
XX	XX	OPERATING SYSTEM: PC-DOS/MS-DOS
XX	XX	SOFTWARE: PatentIn Release #1.0, Version #1.25
XX	XX	CURRENT APPLICATION DATA:
XX	XX	APPLICATION NUMBER: US/08/167,463
XX	XX	FILING DATE: 13-DEC-1993
XX	XX	CLASSIFICATION: 530
XX	XX	ATTORNEY/AGENT INFORMATION:
XX	XX	NAME: LEMHARDT, SUSAN K.
XX	XX	REGISTRATION NUMBER: 33,943
XX	XX	REFERENCE/DOCKET NUMBER: 22000-20542-20
XX	XX	TELECOMMUNICATION INFORMATION:
XX	XX	TELEPHONE: (415) 494-0792
XX	XX	TELEFAX: (415) 494-0792
XX	XX	TELEX: 706141
XX	XX	INFORMATION FOR SEQ ID NO: 10:
XX	XX	SEQUENCE CHARACTERISTICS:
XX	XX	LENGTH: 220 amino acids
XX	XX	TYPE: amino acid
XX	XX	STRANDEDNESS: single
XX	XX	TOPOLOGY: linear
XX	XX	SEQUENCE 220 AA; 24399 MW; 2422975 CN;
DB	33	Score 1643; Match 100.0%; DryMatch 0%; Mismatches 0; Indels 0; Gaps 0;
Matches 220; Conservative 0;		
DB	1	MGAARTLRLAAGLILLATLIRPADACSCSPVHPQQAFCNADVVIRAKAVSEKEVDGND 60
QY	1	YGNPIKRIQYIKQIKMFKEPKDIEFYIATSSAVCGVSLDVGGKEYLAKGAEGDG 120
DB	61	YGNPIKRIQYIKQIKMFKEPKDIEFYIATSSAVCGVSLDVGGKEYLAKGAEGDG 120
QY	61	YGNPIKRIQYIKQIKMFKEPKDIEFYIATSSAVCGVSLDVGGKEYLAKGAEGDG 120

RESULT 2
 ID 05-08-167-463-11 STANDARD; PRT; 220 AA.
 XX
 AC XXXXXX
 XX DT 01-JAN-1900
 XX DE Sequence 11, Application US/08167463.
 XX Sequence 11, Application US/08167463
 CC GENERAL INFORMATION:
 CC APPLICANT: HAWKES, SUSAN P.
 CC APPLICANT: KISHNANI, NARENDR A. S.
 CC APPLICANT: YANG, TE-TUAN
 CC TITLE OF INVENTION: HUMAN TIMP-3
 CC NUMBER OF SEQUENCES: 32
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: MORRISON & FOERSTER
 CC STREET: 755 Page Mill Road
 CC CITY: Palo Alto
 CC STATE: California
 CC COUNTRY: USA
 CC ZIP: 94304-1018
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: PatentIn Release #1.0, Version #1.25
 CC CURRENT APPLICATION NUMBER: US/08/167,463
 CC FILING DATE: 13-DEC-1993
 CC CLASSIFICATION: 530
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: LEHNHARDT, SUSAN K.
 CC REGISTRATION NUMBER: 33,943
 CC REFERENCE/DOCKET NUMBER: 220000-20542.20
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (415) 813-5600
 CC TELEFAX: (415) 494-0792
 CC TELEX: 706141
 CC INFORMATION FOR SEQ ID NO: 11:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 220 amino acids
 CC TYPE: amino acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC SEQUENCE 220 AA; 24367 MW; 243101 CN;
 SQ DB 33; Score 1607; Match 96.8%; QryMatch 97.8%; Pred. No. 1.24e-164;
 Matches 213; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

RESULT 3
 ID US-08-167-463-12 STANDARD; PRT; 220 AA.
 XX
 AC XXXXXX
 XX DT 01-JAN-1900
 XX DE Sequence 12, Application US/08167463.
 CC Sequence 12, Application US/08167463
 CC GENERAL INFORMATION:
 CC APPLICANT: HAWKES, SUSAN P.
 CC APPLICANT: KISHNANI, NARENDR A. S.
 CC APPLICANT: YANG, TE-TUAN
 CC TITLE OF INVENTION: HUMAN TIMP-3
 CC NUMBER OF SEQUENCES: 32
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: MORRISON & FOERSTER
 CC STREET: 755 Page Mill Road
 CC CITY: Palo Alto
 CC STATE: California
 CC COUNTRY: USA
 CC ZFP: 94304-1018
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: PatentIn Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/167,463
 CC FILING DATE: 13-DEC-1993
 CC CLASSIFICATION: 530
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: LEHNHARDT, SUSAN K.
 CC REGISTRATION NUMBER: 33,943
 CC REFERENCE/DOCKET NUMBER: 22000-20542.20
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (415) 813-5600
 CC TELEFAX: (415) 494-0792
 CC TELEX: 706141
 CC INFORMATION FOR SEQ ID NO: 12:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 220 amino acids

CC TYPE: amino acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 SQ SEQUENCE: 220 AA; 24355 MW; 234318 CN;
 DB 33; Score 1550; Match 91.8%; QryMatch 94.3%; Pred. No. 3.16e-158;
 Matches 203; Conservative 12; Mismatches 6; Indels 0; Gaps 0;
 Db 1 MGAAARSLPLAFLCLLGLTLLPDAACSCSPVHPQQAFCNADIVIRAKAVNKEVDGND 60
 Qy 1 MGAAARSLPLAFLCLLGLTLLPDAACSCSPVHPQQAFCNADIVIRAKAVNKEVDGND 60
 Db 61 IYGNP1KR1QYEIKQ1MKF1GPDD1EFTYTAAACVGVS1D1GKEKEYL1JAGRAEGNG 120
 Qy 61 IYGNP1KR1QYEIKQ1MKF1GPDD1EFTYTAAACVGVS1D1GKEKEYL1JAGRAEGDG 120
 Db 121 NMHITLCDF1VPPWDTLSATOKKS1LNHRYQMGECKIT1RCPCMPCY1SSPDEC1MDWVTE 180
 Qy 121 NMHITLCDF1VPPWDTLSATOKKS1LNHRYQMGECKIT1RCPCMPCY1SSPDEC1MDWVTE 180
 Db 181 KNING1QKAFFAC1KRSDGSCAW1RGAAPPKQEF1LD1EDP 220
 Qy 181 KNING1QKAFFAC1KRSDGSCAW1RGAAPPKQEF1LD1EDP 220
 RESULT 4
 ID PCT-US94-14498A-2 STANDARD PRT; 224 AA.
 AC xxxxxxx
 DE 01-JAN-1900
 - Sequence 2, Application PC/TUS9414498A.
 XX
 CC Sequence 2, Application PC/TUS9414498A
 CC GENERAL INFORMATION:
 CC APPLICANT: GREENE, ET AL.
 CC TITLE OF INVENTION: Human TIMP-4
 CC NUMBER OF SEQUENCES: 2
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: CARELLA, STEWART & OLSTEIN
 CC STREET: 6 BECKER FARM ROAD
 CC CITY: ROSELAND
 CC STATE: NEW JERSEY
 CC COUNTRY: USA
 CC ZIP: 07068
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: 3.5 INCH DISKETTE
 CC COMPUTER: IBM PS/2
 CC OPERATING SYSTEM: MS-DOS
 CC SOFTWARE: WORD PERFECT 5.1
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US94/14498A
 CC FILING DATE: Submitted herewith
 CC CLASSIFICATION:
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER:
 CC FILING DATE:
 CC ATTORNEY/AGENT INFORMATION:

CC NAME: FERRARO, GREGORY D.
 CC REGISTRATION NUMBER: 36,134
 CC REFERENCE/DOCKET NUMBER: 32-5800-278
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 201-994-1700
 CC TELEFAX: 201-994-1744
 CC INFORMATION FOR SEQ ID NO: 2:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 224 AMINO ACIDS
 CC TYPE: AMINO ACID
 CC STRANDEDNESS:
 CC TOPOLOGY: LINEAR
 CC MOLECULE TYPE: PROTEIN
 CC SEQUENCE: 224 AA; 25502 MW; 274373 CN;
 DB 4; Score 844; Match 48.2%; QryMatch 51.4%; Pred. No. 2.19e-79;
 Matches 109; Conservative 53; Mismatches 56; Indels 8; Gaps 5;
 Db 1 MGSPREP-SWVLLRLA1RPPGEACSCAPAHPOQHICSAVLTAKTSSEKVP 59
 Qy 1 MGAART1RLA1GLL-LAT1RPA---DACSSEVHPQOAFNADWVTRAKAVSERVD 56
 Db 60 ASADP-ADTERMLRYEIKQ1MKF1GPEKEV1DQ1Y1TPDSSLCVKLEANSOKYLLTG 118
 Qy 57 SNDIYGNP1KR1QYEIKQ1MKF1GPEK---DIEFLYTASSAVGVSLDVGGKEYLLAG 114
 Db 119 QVLSDGKVF1H1CN1YEPWED1S1YORES1NHYLNCGQ1IT1CYT1C1T1C1T1C1W 178
 Qy 115 KAEGDGKMH1T1CDF1VPPWDTLSATOKKS1LNHRYQMGECKIT1RCPCMPCY1SSPDEC1W 174
 Db 179 T1W1L1R1Y1G1Y1Q1H1V1C1S1W1R1G1H1P1R1K1F1V1Q1P 224
 Qy 175 M1W1T1R1N1G1Q1F1A1C1T1R1K1F1C1K1T1P1M1C1Y1S1P1D1E1P1 220
 RESULT 5
 ID PCT-US94-11241-13 STANDARD PRT; 211 AA.
 XX
 AC xxxxxxx
 DE 01-JAN-1900
 - Sequence 13, Application PC/TUS9411241.
 XX
 CC Sequence 13, Application PC/TUS9411241
 CC GENERAL INFORMATION:
 CC APPLICANT: Silbiger, Scott M.
 CC APPLICANT: Koski, Raymond A.
 CC TITLE OF INVENTION: Tissue Inhibitor Metalloproteinase Type
 CC NUMBER OF SEQUENCES: 21
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Amgen Inc./Patent Operations/KMP
 CC STREET: 1840 Dehavenland Drive
 CC CITY: Thousand Oaks
 CC STATE: California
 CC COUNTRY: USA
 CC ZIP: 91300-1789
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patentn Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US94/11241
 CC FILING DATE:
 CC CLASSIFICATION:
 CC INFORMATION FOR SEQ ID NO: 13:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 211 amino acids
 CC TYPE: amino acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQUENCE: 211 AA; 24145 MW; 244095 CN;

DB 4; score 695; Match 43.6%; QryMatch 42.3%; Pred. No. 6.06e-63;
 Matches 95; Conservative 56; Mismatches 55; Indels 12; Gaps 10;

- Db 2 TPWLGLIVLGLWSIGDWGAEACTCPSHQPDAFCNDDIVRAVKVLRGVGP--FGT 59
 | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 - Qy 7 TIRLAIGLLIA-TIL-RPADACSCSPVHPQQAFCNADVIRAKAVSEKEVDSGNDIYN 64

Db 60 -L--V-YTIKOMKMYRGTGKMPHVOYIHEA SE SLCGKLEVN-KYQYLITGRVY-DGRM 113
 :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 - Qy 65 PIKRQQEIKIQIKMFKG-PEK-DIEFTYIAPSACVGSLLDVGKKEYLIAKGADGRM 122

Db 114 YTGLCNMVERWDQITLTSQRKGKLNRYHUGCNCKIKSCSYYLPCFVTSKNECLWTMDSNFG 173
 |:| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 - Qy 123 HITLGDFIVPWTDLSTQPKSLNHYQDGCEKITTRPMIPOYISSLPDECIWMDWTEKN 182

Db 174 YPGYQSKHYACIQRQGCGYCSMWRGAPPDKSIIINATDP 211
 |:| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 - Qy 183 INGHQAKFFACIKRSGSCAWIRGAAPPKQEFLDIEDP 220

RESULT 6
 ID US-08-134-2-31-13 STANDARD; PRT; 211 AA.
 XX XXXXXXXX
 AC XXXXXXXX
 DT 01-JAN-1900
 XX Sequence 13, Application US/08134231.
 CC Sequence 13, Application US/08134231.
 CC GENERAL INFORMATION:
 CC APPLICANT: Silbiger, Scott M.
 CC APPLICANT: Koski, Raymond A.
 CC TITLE OF INVENTION: Tissue Inhibitor Metalloproteinase Type
 CC Three (TIMP-3) Composition and Methods
 CC NUMBER OF SEQUENCES: 21
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Argent Inc./Parent Operations/KMP
 CC STREET: 1840 Dehaviland Drive
 CC CITY: Thousand Oaks
 CC STATE: California
 CC COUNTRY: USA
 CC ZIP: 91320-1789
 CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patentn Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/134,231
 CC FILING DATE:
 CC CLASSIFICATION: 424
 CC INFORMATION FOR SEQ ID NO: 13:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 211 amino acids
 CC TYPE: amino acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQUENCE: 211 AA; 24145 MW; 244095 CN;

DB 30; score 695; Match 43.6%; QryMatch 42.3%; Pred. No. 6.06e-63;
 Matches 95; Conservative 56; Mismatches 55; Indels 12; Gaps 10;

- Db 2 TPWLGLIVLGLWSIGDWGAEACTCPSHQPDAFCNDDIVRAVKVLRGVGP--FGT 59
 | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 - Qy 7 TIRLAIGLLIA-TIL-RPADACSCSPVHPQQAFCNADVIRAKAVSEKEVDSGNDIYN 64

Db 60 -L--V-YTIKOMKMYRGTGKMPHVOYIHEA SE SLCGKLEVN-KYQYLITGRVY-DGRM 113
 :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 - Qy 65 PIKRQQEIKIQIKMFKG-PEK-DIEFTYIAPSACVGSLLDVGKKEYLIAKGADGRM 122

Db 114 YTGLCNMVERWDQITLTSQRKGKLNRYHUGCNCKIKSCSYYLPCFVTSKNECLWTMDSNFG 173
 |:| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 - Qy 123 HITLGDFIVPWTDLSTQPKSLNHYQDGCEKITTRPMIPOYISSLPDECIWMDWTEKN 182

Db 174 YPGYQSKHYACIQRQGCGYCSMWRGAPPDKSIIINATDP 211
 |:| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 - Qy 183 INGHQAKFFACIKRSGSCAWIRGAAPPKQEFLDIEDP 220

RESULT 7
 ID PCT-US94-111599-2 STANDARD; PRT; 211 AA.
 XX XXXXXXXX
 AC XXXXXXXX
 DT 01-JAN-1900
 XX Sequence 2, Application PC/TUS9411599.
 CC Sequence 2, Application PC/TUS9411599
 CC GENERAL INFORMATION:
 CC APPLICANT: Incyte Pharmaceuticals, Inc.
 CC APPLICANT: 3330 Hillview Avenue
 CC APPLICANT: Palo Alto, California 94304
 CC APPLICANT: United States of America
 CC TITLE OF INVENTION: Novel Human Monocyte/Macrophage-Derived
 CC Metalloproteinase Inhibitor, Its Production And Use
 CC NUMBER OF SEQUENCES: 6
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Pennie and Edmonds
 CC STREET: 1155 Avenue of the Americas
 CC CITY: New York

STATE: California
 COUNTRY: United States of America
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/11599
 FILING DATE: 07-OCT-1994
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Halluin, Albert P.
 REGISTRATION NUMBER: 25,227
 REFERENCE/DOCKET NUMBER: 8135-041
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-834-3660
 TELEFAX: 415-854-3694
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 211 amino acids
 TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 IMMEDIATE SOURCE:
 CLONE: T-012006
 SEQUENCE: 211 AA; 24145 MW; 244095 CN;

DB 4; score 695; Match 43.6%; QryMatch 42.3%; Pred. No. 6.06e-63;
 Matches 95; Conservative 56; Mismatches 55; Indels 12; Gaps 10;

Db 2 TPWGLLIVLIGSWLGLDNGAEACTCSPHQPDAFCNNDIVRAKVYGLVKEGP--FGT 59
 Qy 7 TRLALGLLLA-TLL-RPADACSCSPVHPQQQAFCNNDVWIRAKAVSEKEVDSNDIYN 64
 60 -L--V-YTIKOMKMYRGFTKMPHVOYIHEASESILCGIILKEVN-KYQYLITGRVY-DGTM 113
 65 PIKRQYEIKQIRMFKG-PEK-DIEFTYATPSSAVCVSLLDGKKEYLIAKAEGDGRK 122

Db 114 YTGLCNFVERWDQITLISQRKGLNYRYHIGCNCIKTSCKSYLBCFVTSKNECLWDMLSNFG 173
 Qy 123 HITLQDFIVPWTLSITQKSLNHRYQMGCEKTRPMTCYISSPDECWMDWVTERN 182

Db 174 YPGYQSKHAYCIRGKGGSWTRGWWPPDKSIIINATDP 211
 Qy 183 INGHOAKFFACIKRSQDSGCAWTRGAAPFKQEFLDIEDP 220

RESULT 8
 ID US-08-319-555-2 STANDARD PRT; 211 AA.
 XX XXXXXXXX
 AC
 XX
 DT 01-JAN-1900
 XX Sequence 2, Application US/08319555.
 DE

CC Sequence 2, Application US/08319555
 CC GENERAL INFORMATION:
 CC APPLICANT: Scott, Randal W.
 CC APPLICANT: Levine, Wendy B.
 CC APPLICANT: Seilhamer, Jeffrey J.
 CC APPLICANT: Delegane, Angelo M.
 CC TITLE OF INVENTION: Novel Human Monocyte/Macrophage Derived
 CC TITTLE OF INVENTION: Metalloproteinase Inhibitor, Its Production And U
 ses
 CC NUMBER OF SEQUENCES: 4
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Pennie & Edmonds
 CC STREET: 1155 Avenue of the Americas
 CC CITY: New York
 CC STATE: New York
 CC COUNTRY: USA
 CC ZIP: 10036
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/319,555
 CC FILING DATE: 07-OCT-1994
 CC CLASSIFICATION: 435
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/133,956
 CC FILING DATE: 07-OCT-1993
 ATTORNEY/AGENT INFORMATION:
 CC NAME: Halluin, Albert P.
 CC REGISTRATION NUMBER: 25,227
 CC REFERENCE/DOCKET NUMBER: 8135-041-999
 TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 415-854-3660
 CC TELEFAX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 2:
 CC SEQUENCE CHARACTERISTICS:
 LENGTH: 211 amino acids
 TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 SQ SEQUENCE 95; Conservative 56; Mismatches 55; Indels 12; Gaps 10;

Db 2 TPWGLLIVLIGSWLGLDNGAEACTCSPHQPDAFCNNDIVRAKVYGLVKEGP--FGT 59
 Qy 7 TRLALGLLLA-TLL-RPADACSCSPVHPQQAFCNNDVWIRAKAVSEKEVDSNDIYN 64
 60 -L--V-YTIKOMKMYRGFTKMPHVOYIHEASESILCGIILKEVN-KYQYLITGRVY-DGTM 113
 65 PIKRQYEIKQIRMFKG-PEK-DIEFTYATPSSAVCVSLLDGKKEYLIAKAEGDGRK 122

Db 114 YTGLCNFVERWDQITLISQRKGLNYRYHIGCNCIKTSCKSYLBCFVTSKNECLWDMLSNFG 173
 Qy 123 HITLQDFIVPWTLSITQKSLNHRYQMGCEKTRPMTCYISSPDECWMDWVTERN 182

Db 174 YPGYQSKHAYCIRGKGGSWTRGWWPPDKSIIINATDP 211
 Qy 183 INGHOAKFFACIKRSQDSGCAWTRGAAPFKQEFLDIEDP 220

RESULT 8
 ID US-08-319-555-2 STANDARD PRT; 211 AA.
 XX XXXXXXXX
 AC
 XX
 DT 01-JAN-1900
 XX Sequence 2, Application US/08319555.
 DE

Db 174 YPGYOKSHYACIIRQKGCGCSWYRWRAPPKSLINATDP 2111
 Qy 183 INGHOKRFFACIKRSRDGSCAWYRGAAPPKQEFLDIEDP 2200

RESULT 9
 ID US-08-167-463-13 STANDARD; PRT; 212 AA.
 AC xxxxxxxx
 DT 01-JAN-1900
 XX
 DE Sequence 13, Application US/08167463.
 XX
 Sequence 13, Application US/08167463
 CC GENERAL INFORMATION:
 CC APPLICANT: HAWKES, SUSAN P.
 CC APPLICANT: KISHNANI, NARENDRA S.
 CC APPLICANT: YANG, TE-TUAN
 CC TITLE OF INVENTION: HUMAN TIMP-3
 CC NUMBER OF SEQUENCES: 32
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: MORRISON & FORESTER
 CC STREET: 755 Page Mill Road
 CC CITY: Palo Alto
 CC STATE: California
 CC COUNTRY: USA
 CC ZIP: 94304-1018
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC Compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/167,463
 CC FILING DATE: 13-DEC-1993
 CC CLASSIFICATION: 530
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: LEHNHARDT, SUSAN K.
 CC REGISTRATION NUMBER: 33,943
 CC REFERENCE/DOCKET NUMBER: 22000-20542.20
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (415) 813-5600
 CC TELEFAX: (415) 494-0792
 CC TELEX: 706141
 CC INFORMATION FOR SEQ ID NO: 13:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 212 amino acids
 CC TYPE: amino acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 SQ SEQUENCE 212 AA; 24504 MW; 238212 CN;

Db 33 Score 686; Match 45.2%; OryMatch 41.8%; Pred. No. 5.91e-62;
 Matches 90; Conservative 49; Mismatches 50; Indels 10; Gaps 8;

Db 22 AEACTCVP1HPOQAFNSDIVIRAKVVGKKLMDGP--FGT-M-R--YTYKQMKMYRGRQ 75
 Qy 24 ADACSCSPVHPQQAFCNADVTRAKAVSEKEVDSGN1YGNPIKRIQEIKQIRKFKG-P 82

Db 76 IMPHOVQYTYTEASESUCGVKLEVN-KYQYLIGRVY-EGKVYTGICNWTKEWDRITLTSR 133
 Qy 83 EK-DIEFYTASSAVGVSLSVGGKEYLLGKAEQDGKMHITLCDFIVPWTJLSTOK 141
 Db 134 KGLNHRVHLGGCKKIRCPYVYLPCFATSKNECWTMMSNFCHSGHOAKHYACIQRVEGYC 193
 Qy 142 KSLNHRVOMGCKTTRCPMPCYLISSPDECILWMDWTERKNINGQAKPFACIKRSRDGSC 201
 Db 194 SWTRGWAAPPDKTINATDP 212
 Qy 202 AWTRGAAAPPKQEFLDIEDP 220

RESULT 10
 ID US-08-167-463-14 STANDARD; PRT; 211 AA.
 XX
 AC xxxxxxxx
 XX
 DT 01-JAN-1900
 XX
 Sequence 14, Application US/08167463.
 CC GENERAL INFORMATION:
 CC APPLICANT: HAWKES, SUSAN P.
 CC APPLICANT: KISHNANI, NARENDRA S.
 CC APPLICANT: YANG, TE-TUAN
 CC TITLE OF INVENTION: HUMAN TIMP-3
 CC NUMBER OF SEQUENCES: 32
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: MORRISON & FORESTER
 CC STREET: 755 Page Mill Road
 CC CITY: Palo Alto
 CC STATE: California
 CC COUNTRY: USA
 CC ZIP: 94304-1018
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent In Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/167,463
 CC FILING DATE: 13-DEC-1993
 CC CLASSIFICATION: 530
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: LEHNHARDT, SUSAN K.
 CC REGISTRATION NUMBER: 33,943
 CC REFERENCE/DOCKET NUMBER: 22000-20542.20
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (415) 813-5600
 CC TELEFAX: (415) 494-0792
 CC TELEX: 706141
 CC INFORMATION FOR SEQ ID NO: 13:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 212 amino acids
 CC TYPE: amino acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 SQ SEQUENCE 212 AA; 24504 MW; 238212 CN;

Db 33 Score 686; Match 45.2%; OryMatch 41.8%; Pred. No. 5.91e-62;
 Matches 90; Conservative 49; Mismatches 50; Indels 10; Gaps 8;

Db 22 AEACTCVP1HPOQAFNSDIVIRAKVVGKKLMDGP--FGT-M-R--YTYKQMKMYRGRQ 75
 Qy 24 ADACSCSPVHPQQAFCNADVTRAKAVSEKEVDSGN1YGNPIKRIQEIKQIRKFKG-P 82

INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 211 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 SEQUENCE 211 AA; 24182 MW; 246088 CN;

APPLICATION NUMBER: US/08/134,231
 FILING DATE: 4/24
 CLASSIFICATION: 17:
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 164 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE 164 AA; 19117 MW; 146524 CN;
 DB 30; Score 556; Match 41.8%; OryMatch 33.8%; Pred. No. 9.90e-48;
 Matches 66; Conservative 43; Mismatches 45; Indels 4; Gaps 4;
 - - - - -

Db 9 PFGTIVYTIKQMKMYRGFTKMPHYQIHTAESELCKLKEVN-KYQYLITGRVY-DGKRM 66
 Qy 65 PIRKIQYEIKQIRKAFKG-PEK-DIEFIYTAPOSSAVGVSLSLGGKKEYLIAEKGKRM 122
 - - - - -

Db 67 YTGLCNFVERWDQLTISORKGKMYRHYHUGCNKIKSCSYLPCFVSKNECLWTDMSNFG 126
 Qy 123 HITLCDFTIPWDTLSTTORKSLSNHYQMGECKTTRCPMIPYSSDECIMMDWVTEKN 182
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Db 127 YPGYOSKHYACIROLGGYCSWYRGWAPPDKSINATDP 164
 Qy 183 INGHOAKFFACIKRSDDGSOAWTGAAPPKQEFLIEDP 220
 - - - - -

Db 127 YPGYOSKHYACIROLGGYCSWYRGWAPPDKSINATDP 164
 Qy 183 INGHOAKFFACIKRSDDGSOAWTGAAPPKQEFLIEDP 220
 - - - - -

Search completed: Mon Feb 5 17:04:01 1996
 Job time : 118 sec.

RESULT 15
 ID PCT-US94-11241-17 STANDARD; PRT; 164 AA.
 XX
 XX
 AC
 XX
 DT 01-JAN-1900
 XX
 DE Sequence 17, Application PC/TUS9411241.
 XX

Sequence 17, Application PC/TUS9411241

GENERAL INFORMATION:

APPLICANT: Silbiger, Scott M.

APPLICANT: Koski, Raymond A.

TITLE OF INVENTION: Tissue Inhibitor Metalloproteinase Type

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSSEE: Amgen Inc./Patent Operations/KMP
 STREET: 1840 Dehavenland Drive
 CITY: Thousand Oaks
 STATE: California
 COUNTRY: USA
 ZIP: 91320-1789

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/11241

FILING DATE:

CLASSIFICATION:

CC INFORMATION FOR SEQ ID NO: 17:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 164 amino acids
 CC TYPE: amino acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQUENCE 164 AA; 19117 MW; 146524 CN;
 CC Matches 66; Conservative 43; Mismatches 45; Indels 4; Gaps 4;
 - - - - -

Db 9 PFGTIVYTIKQMKMYRGFTKMPHYQIHTAESELCKLKEVN-KYQYLITGRVY-DGKRM 66
 Qy 65 PIRKIQYEIKQIRKAFKG-PEK-DIEFIYTAPOSSAVGVSLSLGGKKEYLIAEKGKRM 122
 - - - - -

Db 67 YTGLCNFVERWDQLTISORKGKMYRHYHUGCNKIKSCSYLPCFVSKNECLWTDMSNFG 126
 Qy 123 HITLCDFTIPWDTLSTTORKSLSNHYQMGECKTTRCPMIPYSSDECIMMDWVTEKN 182
 - - - - -

Db 127 YPGYOSKHYACIROLGGYCSWYRGWAPPDKSINATDP 164
 Qy 183 INGHOAKFFACIKRSDDGSOAWTGAAPPKQEFLIEDP 220
 - - - - -

Search completed: Mon Feb 5 17:04:01 1996
 Job time : 118 sec.

Release 2.1D John F. Collins, Biocomputing Research Unit.
 Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
 Distribution rights by IntelliGenetics, Inc.

MPsearch_pp protein - protein database search, using Smith-Waterman algorithm
 Run on: Mon Feb 5 16:59:25 1996; MasPar time 11.53 Seconds
 482.321 Million cell updates/sec
 Tabular output not generated.

Title: >FIG2
 Description: 1643
 Perfect Score: 1
 Sequence: 1 MGAAARTIRLALGILLATL.....CAWYRGAAAPPKQEFLIEDP 220
 Scoring table: PAM 150
 Gap 11
 - - - - -

Searched: 82306 seqs, 25270970 residues
 Database: Pirs6
 - - - - -

1	ann1
2	ann2
3	ann3
4	unann1
5	unann2
6	unann3
7	unann4
8	unann5
9	unann6
10	unann7
11	unann8
12	unrev1
13	unrev2

Statistics: Mean 42.711; Variance 87.125; scale 0.490

SUMMARIES						
Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	1643	100.0	220	4	A31128 metalloproteinase ti	0.00e+00
2	1630	99.0	220	13	S45683 metalloproteinases-2	2.89e-303
3	1620	98.6	220	4	J06863 metalloproteinase in	3.44e-301
4	1550	94.3	220	4	A35996 metalloproteinase in	1.14e-286
5	1466	89.2	196	4	S38612 metalloproteinase in	2.88e-269
6	1392	84.7	185	4	S21303 metalloproteinase in	5.84e-254
7	695	42.3	211	10	J43317 metalloproteinase ti	1.44e-111
8	686	41.8	212	10	A43429 metalloproteinase in	9.19e-110
9	686	41.8	211	11	A5532 tissue inhibitor of	9.19e-110
10	686	41.8	211	11	S43052 metalloproteinase-3	9.19e-110
11	680	41.4	210	10	S41041 mig Protein - human	1.46e-108
12	677	41.2	198	11	S43053 metalloproteinase-3	5.82e-108
13	676	41.1	197	11	S46114 tissue inhibitor of	9.23e-108
14	521	31.7	207	2	ZYHDEP metalloproteinase ti	5.23e-108
15	518	31.5	206	4	A33350 metalloproteinase in	2.03e-76
16	517	31.5	207	4	S13685 metalloproteinase in	3.19e-76
17	508	30.9	217	13	J2C257 metalloproteinase 1	1.86e-07
18	506	30.8	205	4	A26106 collagenase inhibitio	4.57e-74
19	488	29.7	207	4	A26633 metalloproteinase in	1.51e-74
20	186	11.3	57	10	A35043 21K extracellular ma	1.56e-14
21	172	10.5	31	4	S18428 metalloproteinase in	3.20e-12
22	164	10.0	22	13	S20325 metalloproteinase in	6.35e-11
23	138	8.4	22	13	S20326 metalloproteinase in	7.42e-07
24	122	7.4	21	4	B39120 30K metalloproteinas	1.71e-04
25	117	7.1	29	7	S15198 hydrogenase isozyme	8.78e-04
26	100	6.1	76	11	S25146 CD24 protein - rat	1.74e-01
27	99	6.0	69	7	A21132 gag-abl-pol polyprot	2.34e-01
28	98	6.0	1025	9	S24507 probable membrane pr	3.14e-01
29	96	5.8	141	13	S15785 heat-stable antigen	5.63e-01
30	96	5.8	76	13	S15784 heat-stable antigen	5.63e-01
31	96	5.8	76	11	S43709 heat-stable antigen	5.63e-01
32	96	5.8	76	11	A44537 heat-stable antigen	5.63e-01
33	96	5.8	76	11	S33129 heat-stable antigen	5.63e-01
34	93	5.7	310	10	S33117 d13k protein - human	1.33e+00
35	93	5.7	404	13	B45313 non-coding + transport	1.33e+00

Statistics: Mean 42.711; Variance 87.125; scale 0.490
 n=221
 unrev2 13

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES						
Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	1643	100.0	220	4	A31128 metalloproteinase ti	0.00e+00
2	1630	99.0	220	13	S45683 metalloproteinases-2	2.89e-303
3	1620	98.6	220	4	J06863 metalloproteinase in	3.44e-301
4	1550	94.3	220	4	A35996 metalloproteinase in	1.14e-286
5	1466	89.2	196	4	S38612 metalloproteinase in	2.88e-269
6	1392	84.7	185	4	S21303 metalloproteinase in	5.84e-254
7	695	42.3	211	10	J43317 metalloproteinase ti	1.44e-111
8	686	41.8	212	10	A43429 metalloproteinase in	9.19e-110
9	686	41.8	211	11	A5532 tissue inhibitor of	9.19e-110
10	686	41.8	211	11	S43052 metalloproteinase-3	9.19e-110
11	680	41.4	210	10	S41041 mig Protein - human	1.46e-108
12	677	41.2	198	11	S43053 metalloproteinase-3	5.82e-108
13	676	41.1	197	11	S46114 tissue inhibitor of	9.23e-108
14	521	31.7	207	2	ZYHDEP metalloproteinase ti	5.23e-108
15	518	31.5	206	4	A33350 metalloproteinase in	2.03e-76
16	517	31.5	207	4	S13685 metalloproteinase in	3.19e-76
17	508	30.9	217	13	J2C257 metalloproteinase 1	1.86e-07
18	506	30.8	205	4	A26106 collagenase inhibitio	4.57e-74
19	488	29.7	207	4	A26633 metalloproteinase in	1.51e-74
20	186	11.3	57	10	A35043 21K extracellular ma	1.56e-14
21	172	10.5	31	4	S18428 metalloproteinase in	3.20e-12
22	164	10.0	22	13	S20325 metalloproteinase in	6.35e-11
23	138	8.4	22	13	S20326 metalloproteinase in	7.42e-07
24	122	7.4	21	4	B39120 30K metalloproteinas	1.71e-04
25	117	7.1	29	7	S15198 hydrogenase isozyme	8.78e-04
26	100	6.1	76	11	S25146 CD24 protein - rat	1.74e-01
27	99	6.0	69	7	A21132 gag-abl-pol polyprot	2.34e-01
28	98	6.0	1025	9	S24507 probable membrane pr	3.14e-01
29	96	5.8	141	13	S15785 heat-stable antigen	5.63e-01
30	96	5.8	76	13	S15784 heat-stable antigen	5.63e-01
31	96	5.8	76	11	S43709 heat-stable antigen	5.63e-01
32	96	5.8	76	11	A44537 heat-stable antigen	5.63e-01
33	96	5.8	76	11	S33129 heat-stable antigen	5.63e-01
34	93	5.7	310	10	S33117 d13k protein - human	1.33e+00
35	93	5.7	404	13	B45313 non-coding + transport	1.33e+00

```

ALIGNMENTS

RESULT      1
ENTRY
  TITLE
  ORGANISM
  DATE
    08-Mar-1991 #sequence_revison
    05-Apr-1995
  ACCESSIONS
    A37128; B33996; A34464; A3441
  REFERENCE
  #authors
  Stettler-Stevenson, W.G.; Brown, L.A.
  #journal
  J. Biol. Chem. (1990) 265:137
  #title
  Tissue inhibitor of metalloproteinase expression in tumor cell lines
  #cross-references
  MUID:90338014
  accession
  A37128
  #molecule_type mRNA
  #residues 1-220 #label STE
  #cross-references
  GB:J05593
  REFERENCE
  A35996
  #authors
  Boone, T.C.; Johnson, M.J.; Uhlmann, S.; He, C.; U.S.A.
  #journal
  Proc. Natl. Acad. Sci. U.S.A.
  #title
  cDNA cloning and expression of a cDNA related to tissue inhibitor of metalloproteinase
  #cross-references
  MUID:90207285
  accession
  B35996
  #molecule_type mRNA
  #residues 1-220 #label BCO
  #cross-references
  GB:MM32304
  REFERENCE
  A34464
  #authors
  Stettler-Stevenson, W.G.; Kruijssen, J.; Biol. Chem. (1989) 264:17
  #title
  Tissue inhibitor of metalloproteinase of the metalloproteinase inhibitor
  #cross-references
  MUID:900083902
  accession
  A34464
  #molecule_type protein
  #residues 27-77, 'K', 79-81, 'I', 83-123-149, 'Q', 'L', 151-174, 'I'
  REFERENCE
  A34415
  #authors
  Goldberg, G.I.; Marmer, B.L.; Wilhelm, S.; He, C.; U.S.A.
  #journal
  Proc. Natl. Acad. Sci. U.S.A.
  #title
  Human 72-kilodalton type IV collagen a tissue inhibitor of metalloproteinase
  #cross-references
  MUID:90046765
  accession
  A34415

```

36	93	5.7	383	10	B43484	delta-like dlk homeo	1.33e+00
37	91	5.5	206	3	NB1010	platelet glycoprotein	2.33e+00
38	91	5.5	3033	3	GNWJ8	genome polyprotein -	2.33e+00
39	90	5.5	806	6	A46271	integrin beta p, int	3.08e+00
40	90	5.5	26	4	A42483	gelatinase, 96K - hu	3.08e+00
41	90	5.5	805	6	A42483	integrin beta-7 - chai	3.08e+00
42	90	5.5	806	6	B45203	beta 7 integrin=lymp	3.08e+00
43	89	5.4	361	11	A53860	chondroadherin precu	4.06e+00
44	89	5.4	1036	12	A55974	probable homeobox-do	4.06e+00
44	89	5.4	112	4	B24477	protein-Tyrosine kin	

```

## molecule_type protein
## residues 30-51,124-141,159-173 ##label GOL
GENETICS
#gene GDB:TIMP2
#map Position 17q25
#CLASSIFICATION superfamily metalloproteinase inhibitor
#extracellular protein; proteinase inhibitor
#FEATURES
#domain signal sequence #status experimental #label SIG\

#product metalloproteinase tissue inhibitor 2 #status
#experimental #label MAT
#length 220 #molecular-weight 24399 #checksum 60966

SUMMARY
DB 4; Score 1643; Match 100.0%; QryMatch 100.0%; Pred. No. 0.00e+00; 
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 mgaaartirrlaqlillat1lrpadacs cspvhpgafchadvirakaysekevdsgnd 60
Qy 1 MGAARTIRRLAQLILLAT1LRPADACSCSPVHPQQFCNADVIRAKAYSEKEVDSGND 60

Db 61 iygppkrikqyeikqikmfpkdpkdkiefiytapssavcgvslvdggkkkeylaqkaegcg 120
Qy 61 IYGNPKRIKQYEIKQIKMFPKDPKDKIEFYTAPSSAVCGVSLVDGGKKKEYLAQKAEGCG 120

Db 121 kmhltlcfivpdtd1stqkkslnhrvqmgeckitrcpmipyisstodeclwmdwvte 180
Qy 121 KMHTLCFIVPDTD1STQKKSINHRVQMGECKITRCPMIPYISSPDEC1MDWVTE 180

Db 181 kningqaakffacikrscgscawyrqaaappkgefidiqp 220
Qy 181 KNINGQAAKFFACIKRSQGSCAWYRGAAPPKOEFLDIDP 220

RESULT 2
ENTRY 545683 #type complete
TITLE metalloproteinases-2 - rat
ORGANISM #common name Norway rat
DATE 10-Dec-1994 #sequence_revision 10-Dec-1994 #text_change
10-Dec-1994

ACCESSIONS S45683
REFERENCE Cook, T.F.; Burke, J.S.; Bergman, K.D.; Quinn, C.O.; Jeffrey, J.J.; Partridge, N.C.
#authors Arch. Biochem. Biophys. (1994) 311:313-320
#journal Cloning and regulation of rat tissue inhibitor of
#title metalloproteinases-2 in osteoblastic cells.
#accession S45683
#status preliminary
#residues 1-220 #label COO
#length 220 #molecular-weight 24369 #checksum 63229

SUMMARY
DB 13; Score 1630; Match 98.2%; QryMatch 99.2%; Pred. No. 2.89e-303; 
Matches 216; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 1 mgaaartirrlaqlillat1lrpadacs cspvhpgafchadvirakaysekevdsgnd 60
Qy 1 MGAARTIRRLAQLILLAT1LRPADACSCSPVHPQQFCNADVIRAKAYSEKEVDSGND 60

Db 61 iygppkrikqyeikqikmfpkdpkdkiefiytapssavcgvslvdggkkkeylaqkaegcg 120

```

Db 121 kmhitcdflivpwtlsisqkksinhrqmgceckitrcpmcyisspdclwmdwte 180
 Qy 121 kmhitcdflivpwtlsitqkslnhrqmgceckitrcpmcyisspdclwmdwte 180
 Db 181 ksinghakffaciikrsgdscavrygappaqkgefildedp 220
 Qy 181 KNINQHQAKFFACIKRSGDSCAWYGRAPPKQEFILLEDP 220

RESULT 4 A35996 #type complete
 ENTRY #type complete
 TITLE metalloproteinase inhibitor 2 precursor - bovine
 ALTERNATE_NAMES collagenase inhibitor; tissue inhibitor of metalloproteinases
 (TIMP-2)
 ORGANISM #common name Bos primigenius taurus
 DATE #sequence_revision 16-Nov-1990 #text_change
 05-Apr-1995
 A35996; A34468; A25322; S28151
 ACCESSIONS A35996
 REFERENCE #authors Boone, T.C.; Johnson, M.J.; Langley, K.E.
 #journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:2800-2804
 #title cDNA cloning and expression of a metalloproteinase inhibitor
 related to tissue inhibitor of metalloproteinases.
 #cross-references MUID:9207285
 #accession A35996
 #residues 1-220 #label B00
 #cross-references GB:M32303
 #experimental source aortic endothelium
 REFERENCE A34468
 #authors De Clerck, Y.A.; Yean, T.D.; Batzkin, B.J.; Lu, H.S.;
 Langley, K.E.
 #journal J. Biol. Chem. (1989) 264:17445-17453
 #title Purification and characterization of two related but distinct
 metalloproteinase inhibitors secreted by bovine aortic
 endothelial cells.
 #cross-references MUID:9008914
 #accession A34468
 #status preliminary
 #molecule_type protein
 #residues 27-71 #label DEC
 REFERENCE A25322
 #authors Murray, J.B.; Allison, K.; Suchalter, J.; Langer, R.
 #journal J. Biol. Chem. (1986) 261:4154-4159
 #title Purification and partial amino acid sequence of a bovine
 cartilage-derived collagenase inhibitor.
 #cross-references MUID:86140235
 #accession A25322
 #molecule_type protein
 #residues 27-41, 'C', 43-55, 'EX', 58-59, 'X', 61-66, 'XS', 69-71 #label
 MUR
 #experimental source cartilage
 S28151
 REFERENCE DeClerck, Y.A.; Yean, T.D.; Lee, Y.; Tomich, J.M.; Langley,
 K.E.
 #journal Biochem. J. (1993) 289:65-69
 #title Characterization of the functional domain of tissue inhibitor
 of metalloproteinases-2 (TIMP-2).
 #contents annotation: functional domain
 #classification #superfamily: metalloproteinase inhibitor

KEYWORDS proteinase inhibitor
 FEATURE #domain signal sequence #status predicted #label SIG
 1-26 #product metalloproteinase inhibitor 2 #status predicted
 27-220 #label MAT
 #region inhibitor #status predicted
 SUMMARY #length 220 #molecular_weight 24355 #checksum 3345
 DB 4; Score 1550; Match 91.8%; QryMatch 94.3%; Pred. No. 1.14e-286;
 Matches 202; Conservative 12; Mismatches 6; Indels 0; Gaps 0;
 Db 1 mqaarsplafclllgtllpradacspscphdgafcnadivirkavnkvevdsgnd 60
 Qy 1 MGAARTLRLAIGLILLATLPRADACSCSPVHPQOAFCNADVVTRAKAVSEKEVDSGRD 60
 Db 61 iwynpkrqipekqkikmfkspqdcqdefiytaaaaaavcrysldig9keyliagkaeng 120
 Qy 61 IYNPPIRKIYQETKOKTMFKSPKEKDEFIYTAAPSSAVGVSLSDVCEKKEYLRAEGND 120
 Db 121 mhhitlcfivpwtlsatqkkslnhrqmgceckitrcpmcyisspdclwmdwte 180
 Qy 121 KHRITLCDFIVEWDTLSITOKKSlnHRYQMCCEKITRCMPYISSPDECILWMDWTE 180
 Db 181 kinngqakffaciikrsgdscawrygappaqkgefildedp 220
 Qy 181 KNINQHQAKFFACIKRSGDSCAWYGRAPPQEFILDIEDP 220

RESULT 5 S38624 #type fragment.
 ENTRY metaro proteinase inhibitor, tissue - Chinese hamster
 TITLE (fragment)
 ORGANISM #common name Chinese hamster
 DATE 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
 S38624
 ACCESSIONS S38624
 REFERENCE #authors Suzuki, Y.
 #submission submitted to the EMBL Data Library, November 1993
 #accession S38624
 #status preliminary
 #molecule_type RNA
 #residues 1-196 #label SUZ
 #cross-references EMBL:X75924
 #classification #superfamily metalloproteinase inhibitor
 SUMMARY #length 196 #checksum 7766
 DB 4; Score 1466; Match 99.0%; QryMatch 89.2%; Pred. No. 2.88e-269;
 Matches 193; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Db 2 accscspvhpgqafcnadivirkavsekevdsgndiygnpkriyekgikmfpkpd 61
 Qy 26 accscspvhpgqafcnadivirkavsekevdsgndiygnpkriyekgikmfpkpd 61
 Db 62 iefiytapsavcgvslvdgkkeyliagkaengdgmhltlcfivpwtlsitcqksln 121
 Qy 86 IEFITYTAPSAVCGVSLVDGKKEYLIAGKAENGDMHLTICDFIVPWTLSITQKSLSN 145
 Db 122 hryqmcgeckitrcpmcyisspdclwmdwteksinghakffaciikrsgdscawry 181
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 13 A49614 #type fragment
 ENTRY TITLE A49614 #type fragment of metalloproteinase 3 - human (fragment)
 - ORGANISM #formal_name Homo sapiens #common_name man
 - DATE 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
 -
 ACCESSIONS A49614
 REFERENCE Apte, S. S.; Mattei, M.G.; Olesen, B.R.

RESULT 12 S43053 #type complete
 ENTRY TITLE metalloproteinase-3 tissue inhibitor - mouse
 ORGANISM #formal_name Mus musculus #common_name house mouse
 DATE 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
 13-Jan-1995
 S43053
 REFERENCE Sun, Y.; Hegamyer, G.; Colburn, N.H.
 #authors 54:1139-1144
 #Journal Cancer Res. (1994)
 #title Molecular cloning of five messenger RNAs differentially expressed in preneoplastic or neoplastic JB6 mouse epidermal cells: one is homologous to human tissue inhibitor of metalloproteinases-3.
 #accession S43053
 #status preliminary
 #molecule_type DNA
 #cross-references EMBL:Z30970
 #length 198 #label SUN
 #residues 1-198 #label SUN
 #cross-references EMBL:Z30970
 #molecular_weight 22768 #checksum 1889
 #text_change DB 11; Score 677; Match 44.2%; Pred. No. 5.82e-108;
 Matches 88; Conservative 51; Mismatches 50; Indels 10; Gaps 8;
 -
 Db 8 aeactcspahpqdacfnsdivakvvgkkkvkegp--fgt-1--v-ytikqmkmrygrfgrfs 61
 Qy 24 ADACSCSPVHPQQAFCNADVVIRAKASEKEVDSGNDIYGNPIKRIQYEIKQIKMFKG-P 82
 Db 62 kmphvqyihreasesslcgiklevn-kyqylitgrvy-egkmtyglcnverwhltlsqr 119
 Qy 83 EK-DIEFIYIAPSSAVCGVSLDVGKKEYLIAKGRAGDGRHITLDFIVPWDLTLSTQRK 141
 Db 120 kgliyryhlgcnckikssyy1pofvtksnec1wtmdmlnfngpyqskiyacyirgkgyrc 179
 Qy 142 KSLNHRYQMGCECKTRTPMICYISSPDECILWMDVNTKERNINGHQAKFFACTKRSDDGSC 201
 Db 180 swyrgwappdkksisnatdp 198
 Qy 202 AWIRGAAFPKQEFQFLDIDP 220

RESULT 14 A93353 #type complete
 ENTRY TITLE ZYHUPP #type complete
 ALTERNATE_NAMES tissue inhibitor 1 precursor - human
 ORGANISM #formal_name Homo sapiens #common_name man
 DATE 28-May-1986 #sequence_revision 28-May-1986 #text_change
 A93372; A93363; A22534; A20595; A35826; A01269
 #text_change
 REFERENCE A93372
 #authors Docherty, A.J.P.; Lyons, A.; Smith, B.J.; Wright, E.M.; Stephens, P.E.; Harris, T.J.R.; Murphy, G.; Reynolds, J.J.
 #journal Nature
 #title Sequence of human tissue inhibitor of metalloproteinases and its identity to erythroid-potentiating activity.
 #cross-references MUID:86040463
 #accession A93353
 #molecule_type mRNA
 #residues 1-207 #label DOC
 REFERENCE A93353
 #authors Gasson, J.C.; Golde, D.W.; Kaufman, S.E.; Westbrook, C.A.; Hewick, R.M.; Kaufman, R.J.; Wong, G.G.; Temple, P.A.; Levy, A.C.; Brown, E.L.; Orr, E.C.; Clark, S.C.
 #journal Nature
 #title Molecular characterization and expression of the gene encoding human erythroid-potentiating activity.
 #cross-references MUID:85240567

#accession A93363
 ##molecule_type mRNA
 #residues 1-207 ##label GAS
 REFERENCE A23534
 #authors Carmichael, D.F.; Sommer, A.; Thompson, R.C.; Anderson, D.C.; Smith, C.G.; Welgus, R.C.; Stricklin, G.P.;
 Proc. Natl. Acad. Sci. U.S.A. (1986) 83:2407-2411
 #title Primary structure and cDNA cloning of human fibroblast collagenase inhibitor.
 #cross-references MUID:86205964
 #accession A23534
 #molecule_type mRNA
 #residues 1-207 ##label CAR
 #note parts of this sequence were confirmed by protein sequencing carbohydrate binding sites were determined

REFERENCE A20595
 #authors Stricklin, G.P.; Welgus, H.G.
 #journal J. Biol. Chem. (1983) 258:12232-12258
 #cross-references MUID:84032401
 #accession A20595
 #molecule_type protein
 #residues 24-44, L', 46 ##label STR
 #note six disulfide bonds are present
 REFERENCE A35826
 #authors Rapp, G.; Freudenstein, J.; Klaudiny, J.; Mucha, J.; Wempe, F.; Zimmer, M.; Scheit, K.H.
 #journal DNA Cell Biol. (1990) 9:479-495
 #cross-references MUID:91025550
 #accession A35826
 #molecule_type mRNA
 #residues 1-206 ##label RAP
 #cross-references GB:M38188
 COMMENT This protein, found in a variety of body fluids, complexes with metalloproteinases, irreversibly inactivating them. It also mediates erythropoiesis in vitro, but, unlike IL-3, it is species-specific, stimulating the growth and differentiation of only human and murine erythroid progenitors.
 COMMENT The remarkable heat stability of this protein may be due to disulfide bond formation.

GENETICS
 #gene GDB:TIMP1; CLGI; TIMP
 #map_position Xp11.3-p11.23
 #classifications superfamily metalloproteinase inhibitor; proteinase inhibitor erythropoiesis; glycoprotein; proteinase inhibitor
 #keywords
 #feature 1-13
 #domain signal sequence #status predicted #label SIG
 24-207 #product metalloproteinase inhibitor #status predicted
 #label MAT
 53,101 #binding site carbohydrate (Asn) (covalent) #status experimental
 #length 207 #molecular_weight 23171 #checksum 9750
 #SUMMARY

DB 2; Score 521; Match 41.1%; OryMatch 31.7%; Pred. No. 5.23e-77;
 Matches 81; Conservative 39; Mismatches 70; Indels 7; Gaps 7;

DB 7 lasillllwiapsractcypphptafcnasdvlvirakfvgtpevnqt-lygryeikm 65

QY ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| 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QY 10 IALGILLIATLIRPADACSCSPVHPQQAFCNADVVTRAKVSEKEVSDGNDIYGN-PIKR 68
 Db 66 tk-mykdfqal-gdaacdirfrytpamesvcyfrshnrseeflqagqf-dgllhittc 122
 QY 69 IQEYIKQIKMKGPERDIFTYATPSSAVCVSLDVGGKKE-YLIAKRAEGDGMHITLC 127
 Db 123 sfvpwnsls5qrsqftkyaagcdmctvfacasipchlesdhclwcdss19sd-kgf 182
 QY 128 DFLVPPNTLSITQKSLNHRVYQMGCE-CKITRCMPMPCYISSPDECINMDWWTEKNINGH 186
 Db 183 qsrhlaclpypgkltw 199
 QY 187 QAKFFACIKRSIDGSCAW 203

RA STETTLER-STEVENS W.G., BROWN P.D., ONISTO M., LEVY A.T., LIOTTA L.A.;
 RL J. BIOL. CHEM. 265:13933-13938(1990).
 RN [12]
 RP SEQUENCE FROM N.A.
 RM 90207285
 RA BOONE T.C., JOHNSON M.J., DE CLERCQ Y.A., LANGLEY K.E.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 87:2800-2804(1990).
 RN [13]
 RP SEQUENCE OF 30-214 FROM N.A.
 RA MALIK K., SEIJIMA H., AOKI T., IWATA K.;
 RL SUBMITTED (AUG-1990) TO EMBL/GENBANK/DDJB DATA BANKS.
 RN [14]
 RP SEQUENCE OF 27-219.
 RM 9008902
 RA STETTLER-STEVENS W.G., KRUTZSCH H.C., LIOTTA L.A.;
 RL J. BIOL. CHEM. 264:17374-17378(1989).
 RN [15]
 RP SEQUENCE OF 30-51; 124-141 AND 159-173.
 RM 90046765
 RA GOLDBERG G.I., MARNER B.L., GRANT G.A., EISEN A.Z., WILHELM S., HE C.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 86:8207-8211(1989).
 RN [16]
 RP SEQUENCE OF 27-41.
 RC TISSUE=SYNOVIAL FLUID;
 RM 92111776
 RA KNAUPER V., OBERHOFF R., REINKE H., TSCHESCHE H.;
 RL FEBS LETT. 296:116-20(1992).
 CC -!- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
 CC AND IRREVERSIBLY INACTIVATE THEM.
 CC -!- PTM: THE ACTIVITY OF TIMP-2 IS DEPENDENT ON THE PRESENCE OF
 CC DISULFIDE BONDS.
 CC -!- SIMILARITY: HIGH WITH OTHER MEMBERS OF THE TIMP FAMILY.
 DR EMBL; M32304; HSMET.
 DR EMBL; X54533; HSTIMP2M.
 DR EMBL; A34415; HSTIMP2.
 DR EMBL; A34464; A34464.
 DR PIR; B35916; B35996.
 DR PIR; A37128; A37128.
 DR PIR; S20319; S20319.
 DR PROSITE; PS00288; TIMP.
 KW METALLOPROTEASE INHIBITOR; SIGNAL.
 FT SIGNAL 1 26
 FT CHAIN 27 220 METALLOPROTEASE INHIBITOR 2.
 FT DISULFID 27 98 BY SIMILARITY.
 FT DISULFID 29 127 BY SIMILARITY.
 FT DISULFID 39 152 BY SIMILARITY.
 FT DISULFID 154 201 BY SIMILARITY.
 FT DISULFID 172 193 BY SIMILARITY.
 FT DISULFID 159 164 BY SIMILARITY.
 FT CONFLICT 78 78 M -> K (IN REF. 4).
 FT CONFLICT 82 82 P -> I (IN REF. 4).
 FT CONFLICT 96 96 A -> V (IN REF. 3).
 FT CONFLICT 101 101 S -> E (IN REF. 4).
 FT CONFLICT 118 118 MISSING (IN REF. 4).
 FT CONFLICT 122 122 M -> R (IN REF. 4).
 FT CONFLICT 150 150 M -> Q (IN REF. 4).
 FT CONFLICT 175 175 M -> T (IN REF. 4).
 SQ SEQUENCE 220 AA; 24399 MW; 242975 CN;

DB 7; Score 1643; Match 100.0%; QryMatch 100.0%; Pred. No. 0.00e+00;
 Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 mogaartlrlagllatllrpadacscspvhpgafcnadvvirakavsekevdsgnd 60
 QY 1 MGAARTLRLAGLLATLLRPADACSCSPVHPQAFCNADVVIRAKAVSEKEVDSGND 60
 Db 61 lygnpikrkyeqikqikmfkqpekdiefiytapassavcgvsldvggkeyliaakaedg 120
 QY 61 ICGNPIKRIQEYIKQIKMFKQPEKDIEFIYATPSSAVCGVSLDVGGKEYLIAKAEDG 120
 Db 121 kmbitlcfdfivwqdtlstrtkkslnhrlymgcectrcmcpvissdecwmdwte 180
 QY 121 KKHITLCDFIVWQDTLSTRTKKSLNHRLYQMGCECTRCMCPVISSDECWMDWTE 180
 Db 181 kningqakffaciksdgscawyrqaapkkqefldiedp 220
 QY 181 KNINGQAKFFACIKSDGSCAWYRGAAPPKQEFLDIEDP 220
 RESULT 2
 ID TIM2_MOUSE STANDARD PRT; 220 AA.
 AC P25785;
 DT 01-MAY-1992 (REL 22, CREATED)
 DT 01-APR-1993 (REL 25, LAST SEQUENCE UPDATE)
 DT 01-FEB-1995 (REL 31, LAST ANNOTATION UPDATE)
 DE METALLOPROTEINASE INHIBITOR 2 PRECURSOR (TIME-2)
 DE METALLOPROTEINASES-2).
 GN TIMP-2.
 OS MUS MUSCUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RC SEQUENCE FROM N.A.
 RM 92290292
 RA SHIMIZU S., MALIK K., SEJIMA H., KISHI J.I., HAYAKAWA T., KOIWA O.;
 RL GENE 114:291-292(1992).
 RN [2]
 RC SEQUENCE FROM N.A.
 RM 923477695
 RA LECO K.J., HAYDEN L.J., SHARMA R.R., ROCHELEAU H., GREENBERG A.H.,
 RA EDWARDS D.R.;
 RL GENE 117:209-217(1992).
 RN [3]
 RC PRELIMINARY SEQUENCE OF 27-62.
 RM 91226375
 RA KISHI J.I., OGAWA K., YAMAMOTO S., HAYAKAWA T.;
 RL MAATRIX 11:10-16(1991).
 CC -!- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
 CC AND IRREVERSIBLY INACTIVATE THEM.
 CC -!- PTM: THE ACTIVITY OF TIMP-2 IS DEPENDENT ON THE PRESENCE OF
 CC DISULFIDE BONDS.
 CC -!- SIMILARITY: HIGH WITH OTHER MEMBERS OF THE TIMP FAMILY.
 DR EMBL; X62622; MNTIMP2.
 DR EMBL; M82858; MNTIMP2A.
 DR EMBL; M93954; MNTIMP2B.
 PIR; S15987; S15987.
 DR PIR; JH0683; JH0683.

DR PROSITE; PS00288; TIMP.
 KW METALLOPROTEASE INHIBITOR; SIGNAL.
 FT SIGNAL 1 26
 FT CHAIN 27 220 METALLOPROTEINASE INHIBITOR 2.
 FT DISULFID 27 98 BY SIMILARITY.
 FT DISULFID 29 127 BY SIMILARITY.
 FT DISULFID 39 152 BY SIMILARITY.
 FT DISULFID 154 201 BY SIMILARITY.
 FT DISULFID 172 193 BY SIMILARITY.
 FT DISULFID 159 164 BY SIMILARITY.
 FT CONFLICT 12 12 L -> H (IN REF. 2).
 FT CONFLICT 21 21 V -> L (IN REF. 2).
 FT CONFLICT 195 195 K -> E (IN REF. 2).
 SQ SEQUENCE 220 AA; 24328 MW; 244289 CN;

DB 7; Score 1620; Match 97.3%; OryMatch 98.6%; Pred. No. 0.00e+00; Matches 214; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

DB 1 maaaaarsrlrlalglillla:ivrpadaacspvppqgafcnadvirkavakevksrgnd 60
 Qy 1 MCAAATRLRLALGLILLATLRLPADACSCSPVHPQQAFNCNAADVIRKAVKEVDSGND 60

Db 61 lygnpiakrigeitqkmfkqpkdiefiytapsaacsrgvaldvggkkeyliagkaegdg 120
 Qy 61 IYGNPPTKRTIQYEIKQIKMFKGPEKDIETYTAPSSAVCGVSLDVGSKKEYLIAKGAEGDG 120

Db 121 kmhitlcfdfivpwtdlsltqkkslnhrqmgceckitrcpmcyis spdeclwmdwte 180
 Qy 121 KMHITLCDFIVPWDLTLSTTQKKSLNHRQMGCECKITRCPMCYISSPDECLWMDWTE 180

Db 181 ksnqbqakffacikrsdgscawyrgappkqefldedp 220
 Qy 181 KNINGHQAKFFACIKRSDGSACAWYRGAPPKQEFLDDEDP 220

RESULT 3
 ID TIM2_BOVIN STANDARD; PRT; 220 AA.
 AC P16368;
 DT 01-AUG-1990 (REL. 15, CREATED)
 DT 01-MAY-1991 (REL. 18, LAST SEQUENCE UPDATE)
 DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
 DE METALLOPROTEINASE INHIBITOR 2 PRECURSOR (TIMP-2) (TISSUE INHIBITOR OF
 DE METALLOPROTEINASES-2) (COLLAGENASE INHIBITOR).
 OS BOS Taurus (BOVINE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; ARTIODACTyla.
 RN [1]
 RP SEQUENCE FROM N.A.

PM 90207285
 RA BOONE T.C., JOHNSON M.J., DE CLERCK Y.A., LANGLEY K.E.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 87:2800-2804 (1990).
 RN [2]
 RP SEQUENCE OF 27-71.
 RC TISSUE=CARTRIDGE;
 RM 86140235
 RA MURRAY J.B., ALLISON K., SUDHALTER J., LANGER R.;
 RL J. BIOL. CHEM. 261:4154-4159 (1986).
 RN [3]
 RP SEQUENCE OF 27-71.
 RM 90008914

RA DE CLERCK Y.A., YEAN T.D., RAYKIN B.J., LU H.S., LANGLEY K.E.;
 RL J. BIOL. CHEM. 264:17445-17453 (1989).
 CC -!- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
 CC AND IRREVERSIBLY INACTIVATE THEM.
 CC -!- PTM: THE ACTIVITY OF TIMP-2 IS DEPENDENT ON THE PRESENCE OF
 CC DISULFIDE BONDS.
 CC -!- SIMILARITY: HIGH WITH OTHER MEMBERS OF THE TIMP FAMILY.
 DR EMBL; M32303; BTNET.
 DR PIR; A25222; A25222.
 DR PIR; A35996; A35996.
 DR PIR; A34468; A34468.
 DR PROSITE; PS00288; TIMP.
 KW METALLOPROTEASE INHIBITOR; SIGNAL.
 FT SIGNAL 1 26 METALLOPROTEINASE INHIBITOR 2.
 FT CHAIN 27 220 BY SIMILARITY.
 FT DISULFID 27 98 BY SIMILARITY.
 FT DISULFID 29 127 BY SIMILARITY.
 FT DISULFID 39 152 BY SIMILARITY.
 FT DISULFID 154 201 BY SIMILARITY.
 FT DISULFID 172 193 BY SIMILARITY.
 FT DISULFID 159 164 BY SIMILARITY.
 FT CONFLICT 42 42 D -> C (IN REF. 2).
 FT CONFLICT 56 56 D -> E (IN REF. 2).
 FT CONFLICT 68 68 R -> S (IN REF. 2).
 SQ SEQUENCE 220 AA; 24355 MW; 234318 CN;

DB 7; Score 1550; Match 91.8%; OryMatch 94.3%; Pred. No. 0.00e+00; Matches 202; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

Db 1 maaaaarslplafclllgtlpradacspsvhpgqafcnadvirkavnkkevdsrnd 60
 Qy 1 MAAARTLRLALGLILLATLRLPADACSCSPVHPQQFCNAADVIRKAVSEEVDSGND 60

Db 61 lygnpiakrigeitqkmfkqpkdiefiytapsaacsrgvaldvggkkeyliagkaegng 120
 Qy 61 IYGNPPTKRTIQYEIKQIKMFKGPEKDIETYTAPSSAVCGVSLDVGSKKEYLIAKGAEGDG 120

Db 121 kmhitlcfdfivpwtdlsltqkkslnhrqmgceckitrcpmcyis spdeclwmdwte 180
 Qy 121 KMHITLCDFIVPWDLTLSTTQKKSLNHRQMGCECKITRCPMCYISSPDECLWMDWTE 180

Db 181 ksnqbqakffacikrsdgscawyrgappkqefldedp 220
 Qy 181 KNINGHQAKFFACIKRSDGSACAWYRGAPPKQEFLDDEDP 220

RESULT 4
 ID TIM3_HUMAN STANDARD; PRT; 211 AA.
 AC P35675;
 DT 01-JUN-1994 (REL. 29, CREATED)
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
 DE METALLOPROTEINASE INHIBITOR 3 PRECURSOR (TIMP-3) (TISSUE INHIBITOR OF
 DE METALLOPROTEINASES-3).
 GN
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A..

RC	TISSUE=KIDNEY;
RM	9421520
RA	SILBINGER S.M., JACOBSEN V.L., CUPPLES R.L., KOSKI R.A.;
[2]	GENE 141: 593-297 (1994).
RL	TISSUE=BREAST CARCINOMA;
RN	142
RP	SEQUENCE FROM N.A.
RC	TISSUE=PLACENTA;
RM	94228324
RA	URIA J.A., FERRANDO A.A., VELASCO G., FREIJUE J.M., LOPEZ-OTIN C.;
RL	CANCER RES. 54: 2091-2094 (1994).
[3]	
RN	SEQUENCE OF 14-211 FROM N.A.
RP	SEQUENCE OF 14-211 FROM N.A.
RC	TISSUE=PLACENTA;
RM	94245184
RA	APTE S., MATTEI M., OLSEN B.;
RL	GENOMICS 1: 9-86-90 (1994).
CC	-!- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
CC	-!- SIMILARITY: HIGH WITH OTHER MEMBERS OF THE TIMP FAMILY.
CC	-!- SIMILARITY: HIGH WITH OTHER MEMBERS OF THE TIMP FAMILY.
DR	EMBL; U02571; HS02571;
DR	EMBL; X76522;
DR	EMBL; L15678;
DR	EMBL; HSTIME3A.
PIR	S45317;
DR	PIR; S45317;
DR	MIM; 188826; 11TH EDITION.
DR	PROSITE; PS00288; TIMP.
KW	METALLOPROTEASE INHIBITOR; SIGNAL.
FT	METALLOPROTEASE INHIBITOR; SIGNAL.
FT	1 22 POTENTIAL.
FT	211 METALLOPROTEINASE INHIBITOR 3.
FT	22 SIGNAL.
FT	23 211
FT	24 91
FT	25 118 BY SIMILARITY.
FT	26 143 BY SIMILARITY.
FT	27 143 BY SIMILARITY.
FT	28 192 BY SIMILARITY.
FT	29 155 BY SIMILARITY.
FT	30 184 BY SIMILARITY.
FT	31 22 BY SIMILARITY.
FT	32 22 AE -> R (IN REF. 3).
FT	33 22
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Db 174 Ypsqkskhyacirqkqyqswyrgwappdkseasnacop 211
Qy 183 INGHQAKFFACIKRSQGAAPKQEFIDIEP 220

RESULT 6
ID TIM3 CHICK STANDARD; PRT; 212 AA.
AC E26657;
DT 01-AUG-1992 (REL. 23, CREATED)
DT 01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE METALLOPROTEINASE INHIBITOR 3 PRECURSOR (TIMP-3) (TISSUE INHIBITOR OF METALLOPROTEINASES-3) (21 KD PROTEIN OF EXTRACELLULAR MATRIX).
DE MP-3.
GN GALLUS GALLUS (CHICKEN).
OS EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEognathae; OC
OC HOMO SAPIENS (HUMAN).
RN SEQUENCE FROM N.A.
RN TISSUE=EMBRYO FIBROBLAST;
RN 92381050
RA BAVLOFF N., STASKUS P.W., KISHANANI N.S., HAWKES S.P.;
RN J. BIOL. CHEM. 267:17321-17326 (1992).
RN 121
RN SEQUENCE OF 25-53.
RN TISSUE=FIBROBLAST;
RN 910931162
RA STASKUS P.W., MASIARZ F.R., PALLANCK L.J., HAWKES S.P.;
RN J. BIOL. CHEM. 266:449-454 (1991).
CC -1- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
CC -1- AND IRREVERSIBLY INACTIVATE THEM.
CC -1- SIMILARITY: HIGH WITH OTHER MEMBERS OF THE TIMP FAMILY.
DR EMBL: M94531; GGHMP3A.
DR ETR: A39043; A39043.
DR PROST: P500288; TIMP.
DR METALLOPROTEASE INHIBITOR; SIGNAL.
KW
FT SIGNAL 1 24 METALLOPROTEINASE INHIBITOR 3.
FT CHAIN 25 212 BY SIMILARITY.
FT DISULFID 25 92 BY SIMILARITY.
FT DISULFID 27 119 BY SIMILARITY.
FT DISULFID 37 144 BY SIMILARITY.
FT DISULFID 146 193 BY SIMILARITY.
FT DISULFID 151 156 BY SIMILARITY.
FT DISULFID 164 185 BY SIMILARITY.
SQ SEQUENCE 212 AA; 24504 MW; 238212 CN;

DB 7; Score 686; Match 45.2%; QryMatch 41.8%; Pred. No. 1-77e-142;
Matches 90; Conservative 49; Mismatches 50; Indels 10; Gaps 8;

Db 22 aeactcpvhpqdacfnsdivirakvqkk1mkdgp---fgt-m-r-ytvkqmkmyrgfq
Qy 24 ADACSCSPVHPQQAFCNADVTRAKA7SEKEYDGNPDIYGNPIKRUQYEIKQIRAFKG-P 82

Db 76 imphqyiyteassslcgvklevn-kyaylitgrvy-egkvtgjlonwyekwdr1tsgq 133
Qy 83 EK-DIEFITYTAPSSAVCGVSLDVGGREYLIAKEDGKMHITLCDFIVPWDLSTQK 141

Db 134 kglnhryhlgcckirkpevy1pcfatskneciwtdmlsnfghsgdahkyaciqrveyc 193
Qy

Qy 142 KSLNHRYQMGCECKITRCPCMPCYISSPDEC1ANDWTERNINGHOAKEYFACIKRSQGSC 201
Db 194 svyrgwappdktiintdp 212
Qy 202 AWYRGAAPKQEFIDIEP 220

RESULT 7
ID TIM1 HUMAN STANDARD; PRT; 207 AA.
AC P01033;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE METALLOPROTEINASE INHIBITOR 1 PRECURSOR (TIMP-1) (ERYTHROID DE POTENCIATING ACTIVITY) (EPFA) (TISSUE INHIBITOR OF METALLOPROTEINASES) (FIBROBLAST COLLAGENASE INHIBITOR) (COLLAGENASE INHIBITOR).
GN TIM1 OR TIMP.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERA; PRIMATES.
RN SEQUENCE FROM N.A.
RN 86040463
RA DOCHERTY A.J.P., LYONS A., SMITH B.J., WRIGHT E.M., STEPHENS P.E.,
RA HARRIS T.J.R., MURPHY G., REYNOLDS J.J.;
RN NATURE 318:66-69 (1985).
RN (2)
RN SEQUENCE FROM N.A.
RN 85240567
RA GASSON J.C., GOLE D.W., KAUFMAN S.E., WESTBROOK C.A., HEWICK R.M.,
RA KAUFMAN R.J., WONG G.G., TEMPLE P.A., LEARY A.C., BROWN E.L.,
RA ORR E.C., CLARK S.C.;
RN NATURE 315:768-771 (1985).
RN (3)
RN SEQUENCE FROM N.A.
RN 86205964
RA CARMICHAEL D.F., SOMMER A., THOMPSON R.C., ANDERSON D.C., SMITH C.G.,
RA WELGUS H.G., STRICKLIN G.P.;
RN PROC. NATL. ACADEM. SCI. U.S.A. 83:2407-2411 (1986).
RN (4)
RN SEQUENCE FROM N.A.
RA KACZOREK M., HONRE N., RIBES V., DEHOUX P., CORNET P., CARTWRIGHT T.,
RA STRECKER R.E.;
RN BIO/TECHNOLOGY 5:595-598 (1987).
RN (5)
RN SEQUENCE FROM N.A.
RN TISSUE=OVARI;
RM 91025550
RA RAPP G., FREUDENSTEIN J., KLAUDINY J., MUCHA J., WEMPE F., ZIMMER M.,
RA SCHEIT K.H.;
RN DNA CELL BIOL. 9:479-485 (1990).
RN (6)
RN DISULFIDE BONDS, AND PARTIAL SEQUENCE.
RM 90303199
RA WILLIAMSON R.A., MARISON F.A.O., ANGAL S., KOKLITIS P., PANICO M.,
RA MORRIS H.R., CARNE A.F., SMITH B.J., HARRIS T.J.R., FREEMAN R.B.;
RN BIOCHEM. J. 268:267-274 (1990).
RN (7)
RN SEQUENCE OF 24-38.
RC TISSUE=SYNOVIAL FLUID;

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PM 92111776
 RA OSTHODES A., KNAUPEP V., OBERHOFF R., REINKE H., TSCHESCHE H.;
 RL FEBS LETT. 296:16-20 (1992).
 RN [8]
 RP MUTAGENESIS.
 RM 93041700
 RA C' SHEA M., WILLENBROCK F., WILLIAMSON R.A., COCKETT M.I.;
 RA FREEDMAN R.B., REYNOLDS J.J., DOCHERTY A.J.P., MORELY G.;
 RL BIOCHEMISTRY 31:10146-10152 (1992).
 CC -!- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
 CC AND IRREVERSIBLY INACTIVATE THEM.
 CC -!- FUNCTION: ALSO MEDIATES ERYTHROPOEISIS IN VITRO; BUT, UNLIKE IL-3,
 CC IT IS SPECIES-SPECIFIC, STIMULATING THE GROWTH AND DIFFERENTIATION
 CC OF ONLY HUMAN AND MURINE ERYTHROID PROGENITORS.
 CC -!- PTM: THE ACTIVITY OF TIMP-1 IS DEPENDENT ON THE PRESENCE OF
 CC DISULFIDE BONDS.
 CC -!- SIMILARITY: HIGH, WITH OTHER MEMBERS OF THE TIMP FAMILY.
 DR EMBL; X03124; HSTMPPR.
 DR EMBL; M12670; HSFCL.
 DR EMBL; M59806; HSOGCA.
 DR EMBL; X56940; HSGRL22.
 DR PIR; A01269; ZHDEP.
 DR PIR; A23534; A23534.
 DR PIR; A35826; A35826.
 DR PIR; S20318; S20318.
 DR MIM; 305370; 11TH EDITION.
 DR PROSITE; PS00288; TIMP.
 KW GLYCOPROTEIN; METALLOPROTEASE INHIBITOR; ERYTHROCYTE MATURATION;
 KW SIGNAL.
 FT SIGNAL 1 23
 FT CHAIN 24 207 METALLOPROTEINASE INHIBITOR 1.
 - FT DISULFID 24 93
 FT DISULFID 26 122
 FT DISULFID 26 122
 FT DISULFID 36 147
 FT DISULFID 36 147
 FT DISULFID 150 196
 FT DISULFID 155 160
 FT DISULFID 168 188
 FT CARBOHYD 53 53
 FT CARBOHYD 101 101
 SQ SEQUENCE 207 AA; 23171 MW; 222441 CN;
 DB 7; Score 521; March 41.1%; QryMatch 31.7%; Pred. No. 4.90e-100;
 Matches 81; Conservative 39; Mismatches 70; Indels 7; Gaps 7;
 DB 7 1asg1111wiapsractcypphptafcnasdvlvirakfvapevnht-lyqreikm 65
 10 1AIGL111ATL1RPAADACSCSPVHQOAFCNADVVIRAKA/SEKEVDSGNDIYGN-PIKR 68
 66 tk-mfkqfdal-ghatdirfytpanesvcgyskhsqnseefiagqlr-nghlhitc 122
 69 IQEIKQIKMFKGPKEDIEFITYTAPSSAVCGYSLDVGKKE-YLIAKALGGDKMHTLC 127
 DB 123 sfvwpnslsfqrsqftktyaagcdmctvfacasipchlesdthclwtddsslgasd-kgf 181
 DB 128 DfIVPwDLSLTIQKSLNHRVQMGCE-CKITRCPMIPCYISSPDECILMDWTERNINGH 186
 DB 183 qsrhlaclprepglctw 199
 DB 187 QAKFFACIKRSQGSCAW 203
 Qy 187 QAKFFACIKRSQGSCAW 203
 RESULT 9

RESULT 8
 ID TIMP RABBIT STANDARD PRT; 206 AA.
 AC P206T4;
 DT 01-FEB-1991 (REL. 17, CREATED)
 DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
 DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
 DE METALLOPROTEINASE INHIBITOR 1 PRECURSOR (TIMP-1).
 OS ORYCTOLAGUS CUNICULUS (RABBIT).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; LAGOMORPHA.
 RN [1]
 RP SEQUENCE FROM N A.
 RM 89214135
 RA HOROWITZ S., DAFNI N., SHAPIRO D.L., HOLM B.A., NOTTER R.H.,
 RA QUBLE D.J.;
 RL J. BIOL. CHEM. 264:7092-7095 (1989).
 CC -!- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
 CC AND IRREVERSIBLY INACTIVATE THEM.
 CC -!- PTM: THE ACTIVITY OF TIMP-1 IS DEPENDENT ON THE PRESENCE OF
 CC DISULFIDE BONDS.
 CC -!- SIMILARITY: HIGH, WITH OTHER MEMBERS OF THE TIMP FAMILY.
 DR EMBL; J04712; OSTIMP.
 DR PIR; A33350; A33350.
 DR PROSITE; PS00288; TIMP.
 DR GLYCOPROTEIN; METALLOPROTEASE INHIBITOR; ERYTHROCYTE MATURATION;
 KW SIGNAL.
 FT SIGNAL 1 23
 FT CHAIN 24 206 METALLOPROTEINASE INHIBITOR 1.
 FT DISULFID 24 93 BY SIMILARITY.
 FT DISULFID 26 122 BY SIMILARITY.
 FT DISULFID 36 147 BY SIMILARITY.
 FT DISULFID 150 196 BY SIMILARITY.
 FT DISULFID 155 160 BY SIMILARITY.
 FT DISULFID 168 188 BY SIMILARITY.
 FT CARBOHYD 53 53 POTENTIAL.
 FT CARBOHYD 101 101
 SQ SEQUENCE 206 AA; 22758 MW; 218988 CN;
 DB 7; Score 518; Match 40.1%; QryMatch 31.5%; Pred. No. 2.84e-99;
 Matches 79; Conservative 39; Mismatches 71; Indels 8; Gaps 8;

DB 7 1asg1111wiapsractcypphptafcnasdvlvirakfvapevnht-lyqreikm 65
 Qy 10 1AIGL111ATL1RPAADACSCSPVHQOAFCNADVVIRAKA/SEKEVDSGNDIYGN-PIKR 68
 DB 66 tk-mfkqfdal-ghatdirfytpanesvcgyskhsqnseefiagqlr-nghlhitc 122
 Qy 69 IQEIKQIKMFKGPKEDIEFITYTAPSSAVCGYSLDVGKKE-YLIAKALGGDKMHTLC 127
 DB 123 sfvwpnslsfqrsqftktyaagcdmctvfacasipchlesdthclwtddsslgasd-kgf 181
 Qy 128 DfIVPwDLSLTIQKSLNHRVQMGCE-CKITRCPMIPCYISSPDECILMDWTERNINGH 186
 DB 182 qsrhlaclprepglctw 199
 Qy 187 QAKFFACIKRSQGSCAW 203
 RESULT 9

RESULT 10
 ID TIM1 MOUSE STANDARD; PRT; 205 AA.
 AC P12032; P20064;
 DT 01-OCT-1989 (REL. 12, CREATED)
 DT 01-MAY-1991 (REL. 18, LAST SEQUENCE UPDATE)
 DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
 DB METALLOPROTEINASE INHIBITOR 1 PRECURSOR (TIMP-1) (ERYTHROID
 DE POTENTIATING ACTIVITY) (EPA) (TISSUE INHIBITOR OF METALLOPROTEINASES)
 DE (COLLAGENASE INHIBITOR 16C8 FIBROBLAST) (TPA-INDUCED PROTEIN)
 DB (TPA-S1).
 DB TIMP-1.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOI; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA GEMBET D.R., COULOMBE B., CASTELINO M., SKUP D., WILLIAMS B.R.G.;
 RA EMBO J. 6:651-657 (1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=FLIBROBLAST.
 RM 87238524
 EDWARDS D.R., WATERHOUSE P., HOLMAN M.L., DENHARDT D.T.;
 RA NUCLEAR ACIDS RES. 14:8863-8878 (1986).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J.
 RM 88038821
 RA JOHNSON M.D., HOUSEY G.M., KIRSCHMAYER P.T., WEINSTEIN I.B.;
 RA MOL. CELLI. BIOL. 7:2821-2839 (1987).
 CC -!- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES
 CC AND IRREVERSIBLY INACTIVATE THEM).
 CC -!- FUNCTION: ALSO MEDIATES ERYTHROPOEISIS IN VITRO; BUT, UNLIKE IL-3,
 CC IT IS SPECIES-SPECIFIC, STIMULATING THE GROWTH AND DIFFERENTIATION
 CC OF ONLY HUMAN AND MURINE ERYTHROID PROGENITORS.
 CC -!- PTM: THE ACTIVITY OF TIMP-1 IS DEPENDENT ON THE PRESENCE OF
 CC DISULFIDE BONDS.
 CC -!- INDUCTION: BY VIRUS.
 CC -!- INDUCTION: REGULATED BY TUMOR PROMOTERS AND MITOGENS THROUGH
 CC PROTEIN KINASE C.
 CC -!- SIMILARITY: HIGH WITH OTHER MEMBERS OF THE TIMP FAMILY.
 DR EMBL; M230308; MMETAFAMP1.
 DR EMBL; X041684; MM16C8.
 DR EMBL; M11243; MMTPAS1.
 PIR; A26633; A26633.
 PIR; A26106; A26106.
 PIR; A26917; A26917.
 PIR; A26917; A26917.
 DR PROSITE; PS00288; TIMP.
 KW GLYCOPROTEIN; METALLOPROTEASE INHIBITOR; ERYTHROCYTE NATURATION;
 KW SIGNAL.
 FT SIGNAL 1 24
 FT CHAIN 25 205
 FT FT 25 94
 FT DISULFID 25 94
 FT DISULFID 27 123
 FT DISULFID 37 148
 FT DISULFID 151 197
 FT DISULFID 156 161
 FT METALLOPROTEINASE INHIBITOR 1.
 BY SIMILARITY.
 BY SIMILARITY.
 BY SIMILARITY.
 BY SIMILARITY.
 BY SIMILARITY.

DB 7; Score 506; Match 38.6%; OryMatch 30.8%; Pred. No. 3.16e-96; Matches 76; Conservative 43; Mismatches 70; Indels 8; Gaps 8;

DB 8 lasgillllleisskacosccappahpccafncsdvirakfmgspeineett-lyqrykikm 66
QY 10 IALGILLIATLIREADACSCSPVHPOQFCNADVITRAKASEKVDSDNDIYEN-PIKR 68

DB 67 tk-mlkgfikav-gnaadiryayatpvmesllcgqahksnrsseflitgqlrlr-ngnlhiasc 123
QY 69 IYEIKQIKMFKGPEKIDFIFTYATPSSAVCGYSLDVGGKKE-YLAGKALGDKRMHITLC 127

DB 124 sflybwrtlspaqrafafktyaagcgcctyfpcclsipcklesdthclwicqvlvgs-edy 182
QY 128 DFIVPWTDLSTTOKSLNHRYQMGCE-CKITRCPMICYISSLSPDECILWMDWVTEKNINGH 186

DB 183 qsrhfacbrprnglctw 199
QY 187 QAKFFACIKRSIDGSCAW 203

RESULT 11
ID TIM1 PIG
AC S96214;
DT 01-JUN-1994 (REL. 29, CREATED)
DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DT 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE METALLOPROTEINASE INHIBITOR 1, PRECURSOR (TIMP-1).
OS SUS SCROFA (PIG).
OC EUTHERIA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; ARTIODACTYLA.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=OVARY;
RM S2201478
RA TANAKA T., ANDOH N., TAKEYA T., SATO E.;
RL MOL. CELL. ENDOCRINOL. 83:65-71(1992).
CC -!- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
CC -!- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
CC -!- FUNCTION: INACTIVATE THEM.
CC -!- PTM: THE ACTIVITY OF TIMP-1 IS DEPENDENT ON THE PRESENCE OF
DISULFIDE BONDS.
CC -!- SIMILARITY: HIGH WITH OTHER MEMBERS OF THE TIMP FAMILY.
DR EMBL: S96211; S96211.
DR PROSITE; PS00288; TIMP.
KW GLYCOPROTEIN; METALLOPROTEASE INHIBITOR; ERYTHROCYTE MATURATION;
KW SIGNAL.

FT SIGNAL. 1 23 BY SIMILARITY.
FT CHAIN 24 207 BY SIMILARITY.
FT DISULFID 24 93 BY SIMILARITY.

DB 7; Score 491; Match 39.6%; OryMatch 29.9%; Pred. No. 1.99e-92; Matches 78; Conservative 37; Mismatches 75; Indels 7; Gaps 7;

FT DISULFID 26 122 BY SIMILARITY.
FT DISULFID 36 147 BY SIMILARITY.
FT DISULFID 150 197 BY SIMILARITY.
FT DISULFID 155 160 BY SIMILARITY.
FT DISULFID 168 189 BY SIMILARITY.
FT CARBOHYD 53 53 POTENTIAL.
FT CARBOHYD 101 101 SEQUENCE 207 AM; 23098 MW; 218921 CN;

DB 7; Score 78; Standard; PRT; 22 AA.
ID TIM2 RAT
AC P30121;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE METALLOPROTEINASE INHIBITOR 2 (TIMP-2) (TISSUE INHIBITOR OF
DE METALLOPROTEINASES-2) (FRAGMENT).
GN TIMP-2.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RM 92117618
RA ROSWIT W.T., MCCOURT D.W., PARTRIDGE N.C., JEFFREY J.J.;
RL ARCH. BIOCHEM. BIOPHYS. 292:402-410(1992).
CC -!- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
CC -!- AND IRREVERSIBLY INACTIVATE THEM.
CC -!- PTM: THE ACTIVITY OF TIMP-2 IS DEPENDENT ON THE PRESENCE OF
DISULFIDE BONDS.
CC -!- SIMILARITY: HIGH WITH OTHER MEMBERS OF THE TIMP FAMILY.
DR PIR; S20325; S20325.
DR PROSITE; PS00288; TIMP.
KW METALLOPROTEASE INHIBITOR.
FT NON TER 22 22 SEQUENCE 22 AA; 2374 MW; 2188 CN;

DB 7; Score 164; Match 100.0%; OryMatch 10.0%; Pred. No. 9.30e-15; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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